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(57) Abstract

The present invention is concerned with a method of identifying compounds which selectively modulate expression of polypeptides which are crucial for growth and survival of Candida albicans, which method comprises: (a) contacting a compound to be tested with one or more Candida albicans cells having a mutation in a nucleic acid molecule corresponding to the sequences according to any of claims 1 to 8 which mutation results in overexpression or underexpression of said polypeptides, in addition to contacting one or more wild type Candida albicans cells with said compound, (b) monitoring the growth and/or activity of said mutated cell compared to said wild type; wherein differential growth or activity of said one or more mutated Candida cells is indicative of selective action of said compound on a polypeptide or another polypeptide in the same or a parallel pathway. Also disclosed in the present invention are compounds identified and the sequences themselves which are critical for survival and growth of Candida albicans.

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DRUG TARGETS IN CANDIDA ALBICANS

The present invention is concerned with the identification of genes or functional fragments thereof from *Candida albicans* which are critical for growth and cell division and which genes may be used as selective drug targets to treat *Candida albicans* associated infections. Novel nucleic acid sequences from *Candida albicans* are also provided and which encode the polypeptides which are critical for growth of *Candida albicans*.

Opportunistic infections in immunocompromised hosts represent an increasingly common cause of mortality and morbidity. *Candida* species are among the most commonly identified fungal pathogens associated with such opportunistic infections, with *Candida albicans* being the most common species. Such fungal infections are thus problematical in, for example, AIDS populations in addition to normal healthy women where *Candida albicans* yeasts represent the most common cause of vulvovaginitis.

Although compounds do exist for treating such disorders, such as for example, amphotericin, these drugs are generally limited in their treatment because of their toxicity and side effects. Therefore, there exists a need for new compounds which may be used to treat *Candida* associated infections in addition to compounds which are selective in their action against *Candida albicans*.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are

cumbersome and provide no information about a compounds mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

The present inventors have now identified a range of nucleic acid sequences form *Candida albicans* which encode polypeptides which are critical for its survival and growth. These sequences represent novel targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting expression of such polypeptides and their potential use in alleviating diseases or conditions associates with *Candida albicans* infection.

Therefore, according to a first aspect of the invention there is provided a nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast *Candida albicans* and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 1, 2, 3, 5, 10, 11, 12, 14, 16, 18, 20, 21, 23, 25, 27, 29, 31, 33, 37, 39, 41, 44, 45, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 67, 70, 72, 74, 76, 78, 80, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, 110 and 113, or the sequences of nucleotides identified in Figures 9 to 13.

Whilst the molecules defined herein have been established as being critical for growth and metabolism of Candida albicans, for some of the molecules no apparent functionality has been assigned by virtue of the fact that no functionally related sequences in other prokaryotic or eukaryotic organism can be found in respective databases. Thus, advantageously these sequences may be species specific in which case they may be used be used as selective targets for treatment of diseases mediated by *Candida*

Albicans infection. Thus, in one aspct of the invention the nucleic acid molecules preferably comprise the sequences identified in sequence ID Nos 1, 2, 3, 5, 10, 11, 12, 14, 16, 17, 18, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, and 110 and the corresponding polypeptide sequences identified in Table 1.

Some of sequences according to invention have been assigned a particular function. Nucleic acid molecules according to this aspect of the invention comprise any of the sequences as described in sequence ID Nos, 20, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 65, 70, 72, 74, 76, 78, 80, 81, 83, 85 and 113 and the corresponding polypeptides identified in Table 1

Letters utilised in the nucleic acid sequences according to the invention to represent the genetic code and which are not recognisable as letters of the genetic code signify a position in the nucleic acid sequence where one or more of bases A, G, C or T can occupy the nucleotide position. Representative ambiguity codes used to identify the range of bases which can be used are as follows:

M:	A or C
R:	A or G
W:	A or T
S:	C or G
Y:	C or T
K:	G or T
V:	A or C or G
H:	A or C or T
D:	A or G or T
B:	C or G or T
N:	G or A or T or C

In one embodiment of the above identified aspects

of the invention the nucleic acid may comprise a mRNA molecule or alternatively a DNA and preferably a cDNA molecule.

Also provided by the present invention is a nucleic acid molecule capable of hybridising to the nucleic acid molecules according to the invention under high stringency conditions, such as for example, an antisense molecule.

Stringency of hybridisation as used herein refers to conditions under which polynucleic acids are stable. The stability of hybrids is reflected in the melting temperature (Tm) of the hybrids. Tm can be approximated by the formula:

$$81.5°C + 16.6\ (\log_{10}[Na^+] + 0.41\ (\%G\&C) - 600l/l$$

wherein 1 is the length of the hybrids in nucleotides. Tm decreases approximately by 1-1.5°C with every 1% decrease in sequence homology.

The nucleic acid capable of hybridising to nucleic acid molecules according to the invention will generally be at least 70%, preferably at least 80 or 90% and more preferably at least 95 to 97% homologous to the nucleotide sequences according to the invention.

The DNA molecules according to the invention may, advantageously, be included in a suitable expression vector to express polypeptides encoded therefrom in a suitable host.

The present invention also comprises within its scope proteins or polypeptides encoded by the nucleic acid molecules according to the invention or a functional equivalent, derivative or bioprecursor thereof.

Therefore, according to a further aspect of the invention there is provided a polypeptide which is critical for the growth and survival of Candida

albicans comprising an amino acid sequence of any of Sequence ID Numbers 4, 6 to 9, 13, 15, 19, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 43, 47, 48, 51, 53, 54, 56, 58, 60, 62, 64, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 103, 105, 107, 109, 111, 112, 114 or the sequences illiustrated in Figures 14 or 15.

An expression vector according to the invention includes a vector having a nucleic acid according to the invention operably linked to regulatory sequences, such as promoter regions, that are capable of effecting expression of said DNA fragments. The term "operably linked" refers to a juxta position wherein the components described are in a relationship permitting them to function in their intended manner. Such vectors may be transformed into a suitable host cell to provide for expression of a polypeptide according to the invention. Thus, in a further aspect, the invention provides a process for preparing polypeptides according to the invention which comprises cultivating a host cell, transformed or transfected with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the polypeptides, and recovering the expressed polypeptides.

The vectors may be, for example, plasmid, virus or phage vectors provided with an origin of replication, optionally a promoter for the expression of said nucleotide and optionally a regulator of the promoter. The vectors may contain one or more selectable markers, such as, for example, ampicillin resistance.

Polynucleotides according to the invention may be inserted into the vectors described in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense

nucleic acids may be produced by synthetic means.

In accordance with the present invention, a defined nucleic acid includes not only the identical nucleic acid but also any minor base variations including in particular, substitutions in bases which result in a synonymous codon (a different codon specifying the same amino acid residue) due to the degenerate code in conservative amino acid substitutions. The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given regarding base variations.

The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. They may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting for the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesised *in situ* on the array. (See Lockhart *et al.*, Nature Biotechnology, vol. 14, December 1996 "Expression monitoring by hybridisation to high density oligonucleotide arrays". A single array can contain more than 100, 500 or even 1,000 different

probes in discrete locations.

Advantageously, the nucleic acid sequences, according to the invention may be produced using such recombinant or synthetic means, such as for example, using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from a human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al* (Molecular Cloning: a Laboratory Manual, 1989).

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P or ^{39}S, enzyme labels or other protein labels such as biotin or fluorescent markers. such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using known techniques *per se*.

The polypeptide or protein according to the invention includes all possible amino acid variants encoded by the nucleic acid molecule according to the invention including a polypeptide encoded by said molecule and having conservative amino acid changes. Polypeptides according to the invention further include variants of such sequences, including naturally occurring allelic variants which are substantially homologous to said polypeptides. In this context, substantial homology is regarded as a sequence which has at least 70%, preferably 80 or 90% amino acid homology with the polypeptides encoded by

the nucleic acid molecules according to the invention.

A nucleic acid which is particularly advantageous is one comprising the sequences of nucleotides according to Seq ID Nos 1 and 91 in which are specific to *Candida albicans* with no functionally related sequences in other prokaryotic or eukaryotic organism as yet identified from the respective genomic databases.

Nucleotide sequences according to the invention are particularly advantageous for selective therapeutic targets for treating *Candida albicans* associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth of the *Candida albicans* with reductions of associated illnesses or diseases.

The nucleic acid molecule or the polypeptide according to the invention may be used as a medicament, or in the preparation of a medicament, for treating diseases or conditions associated with *Candida albicans* infection.

Advantageously, the nucleic acid molecule or the polypeptide according to the invention may be provided in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

Antibodies to the protein or polypeptide of the present invention may, advantageously, be prepared by techniques which are known in the art. For example, polyclonal antibodies may be prepared by inoculating a host animal, such as a mouse, with the polypeptide according to the invention or an epitope thereof and recovering immune serum. Monoclonal antibodies may be prepared according to known techniques such as described by Kohler R. and Milstein C., Nature

(1975)256, 495-497.

Antibodies according to the invention may also be used in a method of detecting for the presence of a polypeptide according to the invention, which method comprises reacting the antibody with a sample and identifying any protein bound to said antibody. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilises the GAL4

protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β-galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes.

Further provided by the present invention is one or more *Candida albicans* cells comprising an induced mutation in the DNA sequence encoding the polypeptide according to the invention.

A further aspect of the invention provides a method of identifying compounds which selectively inhibit or interfere with the expression, or the functionality of polypeptides expressed from the nucleotides sequences according to the invention or the metabolic pathways in which these polypeptides are involved and which are critical for growth and survival of *Candida albicans*, which method comprises (a) contacting a compound to be tested with one or more *Candida albicans* cells having a mutation in a nucleic acid molecule according to the invention which mutation results in overexpression or underexpression

of said polypeptides in addition to one or more wild type *Candida* cells, (b) monitoring the growth and/or activity of said mutated cell compared to said wild type wherein differential growth or activity of said one or more mutated *Candida* cells provides an indication of selective action of said compound on said polypeptide or another polypeptide in the same or a parallel pathway.

Compounds identifiable or identified using the method according to the invention, may advantageously be used as a medicament, or in the preparation of a medicament to treat diseases or conditions associated with *Candida albicans* infection. These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

A further aspect of the invention provides a method of identifying DNA sequences from a cell or organism which DNA encodes polypeptides which are critical for growth or survival, which method comprises (a) preparing a cDNA or genomic library from said cell or organism in a suitable expression vector which vector is such that it can either integrate into the genome in said cell or that it permits transcription of antisense RNA from the nucleotide sequences in said cDNA or genomic library, (b) selecting transformants exhibiting impaired growth and determining the nucleotide sequence of the cDNA or genomic sequence from the library included in the vector from said transformant. Preferably, the cell or organism may be any yeast or filamentous fungi, such as for example, *Saccharomyces cervisiae*, *Saccharomyces pombe* or *Candida albicans*.

A further aspect of the invention provides a pharmaceutical composition comprising a compound according to the invention together with a

pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention may be more clearly understood with reference to the accompanying example, which is purely exemplary, with reference to the accompanying drawings wherein:

Figure 1: is an illustration of A) Intergration of the antisense library plasmid (here shown as a linear fragment) at a site (eg. *GAL1* promoter region) within the genome which is non-homologous to the insert DNA. As a result the *GAL1*p region is duplicated and antisense RNA can be formed from GENE X upon induction of *GAL1*p, and B) Intergration due to homologous recombination of the gene insert (GENE X) of an antisense library clone (here shown as a linear fragment) with the homologous gene (gene x) within the *Candida* genome. As a result this gene is duplicated. The first copy of the gene geNE X, is flanked by upstream its endogenous promoter and downstream, oppositely-oriented, the *GAL1* promoter resulting in a so-called "collision construct". Antisense RNA can be formed from GENE X upon induction of *GAL1*p. The second copy of the gene, GEne X, is devoid of a promoter and will not be transcribed.

Figure 2: is an illustration of the vectors used for the preparation of a cDNA antisense library, p*GAL1*PNiST-1, (left) and a genomic library, p*GAL1*PNiST-1 (right).

Figure 3: Growth curves in S-glucose and S-galactose medium of respectively the wild type CAI-4 strain and two transformants (clone 36 and 38) showing antisense induced reduction in growth and overall impaired growth, respectively. Growth curves in S-glucose+maltose and S-galactose+maltose medium of respectively the wild type CAI-4 strain and transformants resulting from antisense library transformation.

Figure 4: is an illustration of promoter activity of the *C. albicans GAL1* promoter in the absence and presence of maltose as a carbon source.

Figures 5: is a Northern blot analysis of *C. albicans* mRNA in wild type and clone 36 using a *SAM2* and a *TEF3* specific probe.

Figures 6: is A) a Northern blot analysis of sequences of *C. albicans* mRNA in wild type and clone 38 using a *RNR1* and an *ACT1* specific probe; and B) Real Time Quantitative PCR

on *C. albicans* mRNA in wild type and clone 38 using a *RNR1* and *ACT1* specific fluorogenic probe.

Figure 7: is a nucleotide sequence of plasmid pGAL1PNiST-1.

Figure 8: is a nucleotide sequence of plasmid pGAL1PSiST-1.

Figure 9: is a nucleotide sequence of clone 38 which has been assigned RNR1 functionally.

Figure 10: is a nucleotide sequence of clone 113g4.

Figure 11: is a nucleotide sequence of clone 207g4

Figure 12: is a nucleotide sequence of clone 66g4.

Figure 13: is a nucleotide sequence of clone 36 which has been assigned Sam2 functionally.

Figure 14: is an amino acid sequence of clone 38.

Figure 15: is an amino acid sequence of clone 36.

Figures 16 to 70 are growth curves of Candida albicans showing antisense induced reduction in growth by inhibition of molecules according to the invention.

Example

Identification of novel drug targets in C. albicans by anti-sense and disruptive integration

The principle of the approach is based on the fact that when a particular C. albicans mRNA is inhibited by producing the complementary anti-sense RNA, the corresponding protein will decrease. If this protein is critical for growth or survival, the cell producing the anti-sense RNA will grow more slowly or will die.

Since anti-sense inhibition occurs at mRNA level, the gene copy number is irrelevant, thus allowing applications of the strategy even in diploid organisms.

Anti-sense RNA is endogenously produced from an integrative or episomal plasmid with an inducible promoter; induction of the promoter leads to the production of a RNA encoded by the insert of the plasmid. This insert will differ from one plasmid to another in the library. The inserts will be derived from genomic DNA fragments or from cDNA to cover-to the extent possible- the entire genome.

The vector is a proprietary vector allowing integration by homologous recombination at either the homologous insert or promoter sequence in the Candida genome. After introducing plasmids from cDNA or genomic libraries into C. albicans, transformants are screened for impaired growth after promoter (& thus anti-sense) induction in the presence of lithium acetate. Lithium acetate prolongs the G1 phase and

thus allows anti-sense to act during a prolonged period of time during the cell cycle. Transformants which show impaired growth in both induced and non-induced media, thus showing a growth defect due to integrative disruption, are selected as well.

Transformants showing impaired growth are supposed to contain plasmids which product anti-sense RNA or mRNAs critical for growth or survival. Growth is monitored by measuring growth-curves over a period of time in a device (Bioscreen Analyzer, Labsystems) which allows simultaneous measurement of growth-curves of 200 transformants.

Subsequently plasmids can be recovered from the transformants and the sequence of their inserts determined, thus revealing which mRNA they inhibit. In order to be able to recover the genomic or cDNA insert which has integrated into the Candida genome, genomic DNA is isolated, cut with an enzyme which cuts only once into the library vector (and estimated approx. every 4096 bp in the genome) and relegated. PCR with primers flanking in the insert will yield (Partial) genomic or cDNA inserts as PCR fragments which can directly be sequenced. This PCR analysis (on ligation reaction) will also show us how many integrations occurred. Alternatively the ligation reaction is transformed to E. coli and PCR analysis is performed on colonies or on plasmid DNA derived thereof.

This method is employed for a genome wide search for novel C. albicans genes which are important for growth or survival.

MATERIALS AND METHODS

Constructi n of pGal1NIST-1

pGAL1PNiST-1 (integrative antisense SfiI-NotI vector)

was constructed as described by Logghe et al., submitted.

Construction of pGAL1PSiST-1

The vector pGAL1PSiST-1 (integrative SfiI-SfiI vector) was created for cloning the small genomic DNA fragments behind the GAL1 promoter. The only difference with pGAL1PNiST-1 is that the hIFNb insert fragment in pGAL1PSiST-1 is flanked by two SfiI sites instead of a SfiI and a NotI site as in pGAL1PNiST-1. To construct pGAL1PSiST-1 the EcoRI-HindIII fragment, containing hIFNb flanked by a SfiI and a NotI site, of pMAL2pHiET-3 (Logghe M., unpublished) was exchanged by the EcoRI-HindIII fragment, containing hIFNb flanked by two SfiI sites, from YCp50S-S (an E. coli / S. cerevisiae shuttle vector derived from the plasmid YCp50, which is deposited in the ATCC collection (number 37419; Thrash et al., 1985); an EcoRI-HindIII fragment, containing the gene hIFNb, which is flanked by two SfiI sites, was inserted in YCp50, creating YCp50S-S), resulting into plasmid pMAL2PSiST-1. The MAL2 promoter from pMAL2PSiST-1 (by a NaeI-FspI digest) was further replaced by the GAL1 promoter from pGAL1PNiST-1 (via a XhoI-SalI digest), creating the vector pGAL1PSiST-1.

Preparation of C. albicans genomic library

A C. albicans genomic DNA library with small DNA fragments was prepared for integrative disruption. Genomic DNA of C. albicans B2630 (ATCC No. 44858) was isolated following a modified protocol of Blin and Stafford (1976). To obtain enrichment for genomic DNA fragments of the desired size, the genomic DNA was partially digested. Enrichment of small DNA fragments

was obtained with 70 units of AluI on 10 mg of genomic DNA for 20 min. T4 DNA polymerase (Boehringer) and dNTPs (Boehringer) were added to polish the DNA ends. After extraction with phenol-chloroform the digest was size-fractionated on an agarose gel. The genomic DNA fragments with a length of 0.5 to 1.25 kb were eluted from the gel by centrifugal filtration (Zhu et al., 1985). SfiI adaptors (5' GTTGGCCTTTT) were attached to the DNA ends (blunt) to facilitate cloning of the fragments into the vector. After ligation of these adaptors to the DNA fragments a second size-fractionation was performed on an agarose gel. The small genomic DNA fragments were cloned upstream of the GAL1 promoter in the vector pGAL1PSiST-1. Qiagen-purified pGAL1PSiST-1 plasmid DNA was digested with SfiI and the largest vector fragment eluted from the gel by centrifugal filtration (Zhu et al., 1985). The ligation mix was electroporated to MC1061 (...) E. coli cells.

C. albicans cDNA library

Total RNA was extracted from C. albicans strain B2630 grown on respectively minimal (SD) and rich (YPD) medium as described by Sambrook et al. (1989). mRNA was prepared from total RNA using the Invitrogen Fast Track procedure. First strand cDNA was synthesised with Superscript Reverse Transcriptase (BRL) and with an oligo dT-NotI Primer adapter. After second strand synthesis, cDNA was polished with Klenow enzyme and purified over a Sephacryl S-400 spin column. Phosphorylated SfiI adapters were then ligated to the cDNA, followed by digestion with the NotI restriction enzyme. The SfiI/NotI cDNA was purified and sized on a Biogel column A150M. cDNA was ligated in a NotI/SfiI opened pGAL1PNiST-1 vector.

Transformation of C. albicans

C. albicans CAI-4 (URA3::imm434/URA3::imm434) was kindly provided by Dr. William Fonzi, Georgetown University (Fonzi and Irwin, 1993). CAI-4 was transformed with above described cDNA library or genomic library using a modified spheroplast method (Logghe M., submitted). Cells were plated on minimal medium supplemented with glucose and sorbitol (SD (0.67% Yeast Nitrogen base w/o amino acids + 2% glucose), 1 M sorbitol) plates using 0.4 cm glass-pearls (Glaverbel, Belgium) and incubated for 2-3 days at 30°C.

Screening for mutants

Starter cultures were set up by inoculating each colony in 1 ml SD medium and incubating overnight at 30°C and 300 rpm. Cell densities were determined using a Coulter counter (Coulter Z1; Coulter electronics limited). 250.000 cells/ml were inoculated in SD medium for a total volume of 1ml and cultures were incubated for 24 hours at 30°C and 300 rpm. Cultures were washed in minimal medium without glucose (S) and the pellet resuspended in 650 ml S medium. 8 µl of this culture was used for inoculating 400 µl cultures in a Honeywell-100 plate (Bioscreen analyzer, Labsystems). Each transformant was grown for three days in S medium containing 50 mM LiAc; pH 6.0, with 2% glucose +/- 2% maltose or 2% galactose +/- 2% maltose respectively while shaking (high intensity) every 3 minutes for 20 seconds. Optical densities were measured every hour and growth curves were generated automatically (Bioscreen analyzer; Labsystems).

Construction of LAC4/ pGAL1PNiST-1

pGAL1PNiST-1 vector was cut with StuI in order to release the stuffer fragment and subsequently dephosphorylated (CIP, Boehringer). Plasmid pRS1004, obtained from J. Ernst (University of Duesseldorf, Germany), was cut with PvuII/XbaI in order to release the K. lactis ß-galactosidase (EC 3.2.1.23; LAC4) reporter gene and Klenow-treated. The LAC4 PvuII/XbaI blunted reporter gene fragment from pRS1004 was ligated into StuI opened pGAL1PNiST-1 resulting in the integrative plasmid LAC4/ pGAL1PNiST-1

Measurement of GAL1 promoter activity

C. albicans strain CAI-4 was transformed with LAC4/pGAL1pNiST-1 using the modified spheroplast method (Logghe et al., submitted). Resulting transformants were grown in 5 ml of respectively non-induction (SD +/- maltose) and induction (S+ galactose +/- maltose) medium and further processed as described by Leuker et al. (1997).

Isolation of genomic or cDNA inserts

Potentially interesting transformants were grown in 1.5 ml SD overnight. Genomic DNA was isolated using the Nucleon MI Yeast kit (Amersham) and the concentration of genomic DNA was estimated by analyzing a sample on a 0.7% agarose gel in 0.5x TBE and comparison to a known standard molecular weight marker. 20 ng of genomic DNA was digested for three hours with an enzyme that cuts uniquely in the library vector (SacI for the genomic library; PstI for the cDNA library), treated with RNAse A (Boehringer) and incubated for 20 minutes at 65°C to inactivate the enzyme. Samples were phenol/chloroform extracted twice and precipitated using NaOAc/ethanol. The resulting

pellet was resuspended in 500 µl ligation mixture (1 x ligation buffer and T4 DNA ligase; both from Boehringer) and incubated overnight at 16°C.
After denaturation (10 min 65°C), purification (phenol/chloroform extraction) and precipitation (NaOAc/ethanol) the pellet was resuspended in 10 µl MilliQ (Millipore) water.
Inverse PCR was performed on 1 µl of the precipitated ligation reaction using library vector specific primers (Figure 1) (3pGALSistPCR: 5' GAG-GGC-GTG-AAT-GTA-AGC-GTG 3' and 5pGALNistPCR: 5'GAG-TTA-TAC-CCT-GCA-GCT-CGA-C 3' for the genomic library; 3pGALNistPCR: 5' TGA-GCA-GCT-CGC-CGT-CGC-GC 3' and 5pGALNistPCR for the cDNA library; all primers from Eurogentec) for 30 cycles each consisting of (a) 1 min at 95 °C, (b) 1 min at 61 (or 57 °C for the cDNA library primers), and (c) 3 min at 72 °C. In the reaction mixture 2.5 units of Taq polymerase (Boehringer) with TaqStart antibody (Clontech) (1:1) were used, and the final concentrations were 0.2 µM of each primer, 3 mM $MgCl_2$ (Perkin Elmer Cetus) and 200 µM dNTPs (Perkin Elmer Cetus). All PCR reactions were performed in a Robocycler (Stratagene).
PCR analysis is also performed on genomic DNA isolated from the transformants using primers 3pGALSistPCR and 5pGALNistPCR for the genomic library transformants and using primers oligo23': 5' TGC-AGC-TCG-ACC-TCG-AGG 3' and oligo25: 5' GCG-TGA-ATG-TAA-GCG-TGA-C 3' (T_{hybr} = 53 °C) for the cDNA library transformants.
Resulting PCR products were purified using the PCR purification kit (Qiagen) and were quantified by comparison of band intensity with the intensity of DNA marker bands on a ethidium bromide stained agarose gel.

Sequence determination

The amount of PCR product (expressed in ng) put in the sequencing reaction is calculated as the length of the PCR product in basepairs divided by 10. DNA sequencing reactions were performed using the ABI Prism BigDye Terminator Cycle Sequencing Ready Reaction Kit according to the instructions of the manufacturer (PE Applied Biosystems, Foster City, CA) except for the following modifications. The total reaction volume was reduced to 15 µl. Reaction volumes of individual reagents were changed accordingly. The 6.0 µl Terminator Ready Reaction Mix was replaced by a mixture of 3.0 µl Terminator Ready Reaction Mix + 3.0 µl Half Term (GENPAK Limited, Brighton, UK). After cycle sequencing, reaction mixtures were purified over Sephadex G50 columns prepared on Multiscreen HV opaque Microtiter plates (Millipore, Molsheim, Fr) and were dried in a speedVac. Reaction products were resuspended in 3 µl loading buffer. Following denaturation for 2 min at 95°C, 1 µl of sample was applied on a 5% Long Ranger Gel (36 cm well-to-read) prepared from Singel Packs according to the supplier's instructions (FMC BioProducts, Rockland, ME). Samples were run for 7 hours 2X run on a ABI 377XL DNA sequencer. Data collection version 2.0 and Sequence analysis version 3.0 (for basecalling) software packages are from PE Applied Biosystems.

Sequence analysis

Nucleotide sequences were imported in the VectorNTI software package (InforMax Inc, North Bethesda, MD, USA), and the vector and insert regions of the sequences were identified. Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul et al., 1990) version 1.4. Both the original nucleotide sequence and the six-frame conceptual translations of the insert region were used

as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser et al., 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES Candida albicans sequence database (Stanford University, University of Minnesota). The commercial sequence databases used were the LifeSeq® human and PathoSeq™ microbial genomic databases (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA), and the GENESEQ patent sequence database (Derwent, London, UK). Three major results were obtained on the basis of the sequence similarity searches: function, novelty, and specificity. A putative function was deduced on the basis of the similarity with sequences with a known function, the novelty was based on the absence or presence of the sequences in public databases, and the specificity was based on the similarity with vertebrate homologues.

The 5' UTR region of the SAM2 gene was analysed using the "Findpatterns" algorithm of the Genetics Computer Group (GCG) software package (University of Wisconsin, USA).

Northern blot analysis

Cells were grown to OD_{600} ~ 1.0 and total RNA was prepared using the RNeasy midi kit (Qiagen) according to the manufacturer's instructions. RNA concentrations were determined spectrophotometrically by measuring optical densities at 260 nm in a UV-1601 UV-visible spectrophotometer (Shimadzu) and 5 µg of each sample was resolved onto a 1% formaldehyde gel and run in 1 x formaldehyde gel running buffer (5prime-3prime) at 3.5 V/cm. RNA was stained for 20 minutes using SYBR Green II stain (Molecular probes) 1/10000 diluted in 1x formaldehyde gel running buffer (5prime-3prime) and subsequently transferred to Hybond-N+ nylon membrane (Amersham) by overnight capillary blotting in 20 x

SSC. DIG-labeled probes were prepared using DIG-dUTP (Boehringer Mannheim) at a 1:3 or 1:6 dTTP:DIG-dUTP ratio, 10 pg of template plasmid DNA, 1x PCR buffer II (Perkin Elmer Cetus), 10 µM of each primer (Eurogentec), 0.2 mM of dATP, dCTP and dGTP (Perkin Elmer Cetus), 2.5 mM $MgCl_2$ (Perkin Elmer Cetus), 5% DMSO and 1.25 units Taq polymerase (Boehringer). The membrane was prehybridized at 50°C (DNA probes) or at 68°C (RNA probes) in DIG Easy Hyb (Boehringer Mannheim) for minimum 1 hour. Hybridization was performed using 1 µl PCR reaction product (= 1/50 of the total volume)/ml DIG Easy Hyb. The probes were denatured by heating the PCR reaction for 10 minutes at 96°C, then quick-chilling on ice. The probe was kept on ice for 5 minutes, centrifuged briefly and diluted in pre-warmed DIG Easy Hyb solution. The entire probe solution was filtered through a 0.45 µm filter (Millex HV, Millipore) prior to use. Hybridizations were carried out overnight.
Post-hybridization, membranes were washed twice 15 minutes with 2x SSC/0.1% SDS at room temperature and twice 15 minutes with 0.1x SSC/0.1% SDS at 68°C. Detection was performed using the DIG Wash and Block Buffer Set as described by the manufacturer (Boehringer Mannheim Mannheim) and the blot was exposed to Kodak XAR-5 film for 1 hour at ambient temperature.

Real time quantitation of mRNA transcript
PCR quantitations using specific primers and probes were performed according to the TaqMan procedure (Livak et al., 1995; Orlando et al., 1998) using the ABI Prism 7700 sequence detector (Applied Biosystems). Primers and probes for ACT1 (b-actin) and RNR1 genes were designed using the PrimerExpress software system (Perkin Elmer Cetus).

Cells were grown to OD_{600} ~ 1.0 and total RNA was prepared using the RNeasy midi kit (Qiagen) according to the manufacturer's instructions. All RNA samples were DNaseI (Boehringer-Mannheim, RNAse-free)-treated at 20 U/μg in 50 μl solution for 40 min at ambient temperature, phenol/chloroform-extracted and precipitated. Pellets were dissolved in 20 ml MilliQ water (Millipore) and RNA concentrations were determined spectrophoto-metrically. First-strand cDNA synthesis was performed in a final volume of 20 μl containing 1x Superscript RT buffer (Life Technologies), 10 mM DTT, 125 μM of each dNTP, 50 μM hexamer primers (Life Technologies) and 1 mg RNA. Mixtures were incubated for 10 min. at ambient temperature and 1 μl was removed and diluted 1:4 for the non-amplification control (NAC); 20 U Superscript reverse transcriptase (Life Technologies) was added and the reaction was incubated for 1 hour at 42 °C. The enzyme was inactivated for 10 min at 70°C. PCR reactions were set up in triplicate for all genes and contained 5 ml PCR buffer A, 4 mM $MgCl_2$, 200 μM each of dATP, dGTP, dCTP and 400 μM dUTP, 250 nM fluorogenic probe (for RNR1: 5' TGA-TCT-CAA-AAA-GTG-CTG-GAG-GAA-TCG-GT 3'), 0.5 U UNG, 1.25 U AmpliTaq Gold, 16.75 ml H_2O, 300 nM of appropriate FORWARD (for RNR1: 5' CGA-CAC-TTT-GAA-ATC-GTG-TGC-T 3') and REVERSE (for RNR1: 5' GCA-CCG-GTA-GAA-CGA-ATG-TTG 3') PCR primers, 1 ml of the RT reaction mixture.

For the NAC, 1 μl of the 1:4 diluted RTase-negative sample was added while 1 μl of H_2O was added to each non-template control sample. The ABI PRISM 7700 was run for 50 cycles of 15 s at 95°C, 1 min at 60°C. These cycles were preceded by 5 min at 50°C (UNG activation) and 10 min at 95°C (UNG inactivation and DNA denaturation).

Data were analyzed using the ABI PRISM 7700 software package. Data were normalized according to ACT1 C_T

values.

Library screening

Using primers 5pGalNistPCR and 3pGalNistPCR, a 0.6 kb region of the C. albicans SAM2 gene was PCR-amplified from a SAM2/pGAL1pNiST-1 construct isolated from clone 36 and labeled with [^{32}P]dCTP using the Multiprime™ random-primed labeling system (Amersham). C. albicans genomic DNA isolated from strain B2630 was partially digested with Sau3AI, resolved on a 0.7% agarose gel and the region of the gel with the fragment size of interest (10-23kb) was cut out and DNA was eluted from the gel with Sephaglass Band Prep kit (Pharmacia). A C. albicans library in pYCP50 was prepared by ligating these fragments into a BamHI cut and dephosphorylated pYCP50 vector in a 1:2 molar ratio vector to insert. The titer (#colonies/μg DNA) was determined by transforming a fraction of the library to E. coli. Five genome equivalents were plated out and filter-lifts were prepared as described (Sambrook et al., 1989). Duplicate nylon filters were pre-washed for 2 hours at 42°C in 50 mM Tris, 1M NaCl, 0.1% SDS, 1 mM EDTA to reduce background hybridization. The filters were subsequently hybridized at 42°C overnight in 5x SSPE, 50% formamide, 5x Denhardt's solution, 0.1% SDS, 100 μg/ml denatured salmon sperm DNA and 10^6 cpm/ml of denatured probe. Filters were then washed in 2x SSC, 0.5 % SDS for 1 hour at room temperature and for 1 hour at 50°C. A few intense autoradiographic spots were found and the corresponding colonies were selected for plasmid preparation. Candidate clones were digested with a panel of restriction enzymes, resolved on a 0.7 % agarose gel, stained with ethidiumbromide and transferred to nylon membrane by vacuum-blotting. The blot was probed under the same conditions as the genomic library. A 1.1 kb HpaI

fragment covering the entire hybridizing segment was subcloned into pCR-Blunt (Invitrogen)

Screening for compounds modulating expression of polypeptides critical for growth and survival of C. albicans

The method proposed is based on observations (Sandbaken et al., 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalysing that step and/or less potent against a cell containing an excess of that macromolecule, as compared to the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken et al.). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) C. albicans strain, in the presence of R-

compounds. Strains can be ones in which the expression of a specific essential protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An in silico approach to finding novel essential genes in C. albicans will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth screening.

Assay for High Throughput screening for drugs

35 μl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 μl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected C. albicans strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C. The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C. For the parent strain, CAI-4, the medium is always supplemented with 20 μg/ml uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final PD of 0.24 (+/- 0.04) 6nM is reached.

200 μl of this yeast suspension is added to all

wells of MW96 plates containing R-compounds in a 450 µl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (Y) strains. The ratio (x/y) of these derived variables is calculated.

RESULTS

A C. albicans integrative vector, pGAL1PSiST-1, was constructed to allow non-directional cloning of C. albicans genomic DNA fragments (Figure 2). The vector contains an inducible GAL1 promoter, a SfiI-cloned stuffer fragment, a C. albicans URA3 selection marker and elements to allow autonomous replication and selection in E coli. A C. albicans genomic DNA library was prepared by ligating small genomic DNA fragments (400 to 1000 bp) which were linked to SfiI adaptors into the SfiI opened vector pGAL1PSiST-1 vector. Genomic DNA fragments (450 ng) were ligated into the pGAL1PSiST-1 vector (20 ng). After electroporation into E. coli approximately 400,000 clones were obtained. Plasmid DNA was prepared of … clones; 91% contained an insert with an average length of 600 bp. The size of the library corresponds to over 5 times the diploid genome with genomic DNA inserts oriented in sense or antisense direction in the vector.

A similar C. albicans integrative vector, pGAL1PNiST-1, was constructed to allow SfiI/Not I directional cloning of C. albicans cDNA fragments (Figure 2). The SfiI/NotI cDNA was purified and sized on a Biogel column A150M. The first fraction contained approximately 38,720 clones upon transformation to E. coli with an average insert size of 1500 bp. cDNA from this fraction was ligated into a NotI/SfiI opened pGAL1PNiST-1 vector.

C. albicans strain CAI-4 was transformed with the aforementioned genomic and cDNA libraries. Upon homologous recombination between the insert (partial or complete gene) in a library clone and the corresponding gene in the Candida genome, this gene is (partially if the gene is not full-length) duplicated (Figure 1). The first copy of the gene is flanked upstream by its native promoter and downstream by the GAL1 promoter. The direction of transcription from the native promoter is opposite to that of the GAL1 promoter. Induction of the GAL1 promoter might thus lead to altered expression of the gene at the integration site. Moreover, if the cDNA does not contain the entire 5' coding region, the first copy of the gene may not give rise to any more to a functional protein. The second copy of this gene has lost its promoter and will therefore not be transcribed (Figure 1).

Upon integration at the site of the GAL1 promoter, the promoter is duplicated yielding an integrated gene fragment under control of the GAL1 promoter (Figure 1).

Growth curves were measured in the presence of lithium acetate. Figure 3 shows growth curves of the wild type CAI-4 strain and transformants -resulting from cDNA library transformation- showing either an overall impaired growth (clone 38; Figure 3C) or galactose-induced (clone 36; Figure 3B) reduction in growth. This analysis was performed in S-glucose medium as a non-induction medium and S-galactose medium as an induction medium. The results shown in Figure 3A show that also the wild type strain shows reduced growth in antisense induction medium. This is because galactose is used rather inefficiently as a carbon source by C. albicans. In order to solve this problem and facilitate the selection procedure an extra carbon source, maltose, was added to both inducing and non-inducing medium. Again growth patterns varied significantly from transformant to transformant but growth of the parental strain CAI-4

was nearly identical in both media (Figure 3D). Strains impaired in growth upon promoter activation showed a clear shift in the growth curve in medium supplemented with both galactose and maltose (clone 415; Figure 3E). Overall impaired growth was, as expected, not strongly influenced by the addition of maltose (clone 360; Figure 3F).

To verify that maltose as an extra carbon source did not affect the strength and inducibility of the GAL1 promoter, promoter activity was measured using Kluyveromyces lactis LAC4 reporter gene expression. CAI-4 was transformed with LAC4/pGAL1pNiST-1. Four individual transformants (named Q, R, S, T) were grown in glucose, galactose, glucose+maltose and galactose+maltose media and ß-galactosidase activity was measured (Figure 4). It is clear that the presence of maltose does not significantly influence the induction ratio of the GAL1 promoter.

From a total of over 2000 transformants screened, 198 (~10%) showed an impaired growth phenotype and were selected for further analysis. Fourty-three % of these slow growers showed a growth pattern corresponding with a putative promoter interference or antisense effect, 57% showed overall impaired growth. PCR analysis with 5pGALNiSTPCR and 3pGALNiSTPCR primers on genomic DNA from the transformants can reveal integration outside the gene showing sequence identity with the insert DNA, eg. at the GAL1 promoter region (Figure 1). Of all transformants screened by PCR using these primers, ~ 11% showed integration at a non-insert location.

When the insert of an antisense library clone recombines with the homologous gene in the C. albicans genome, no PCR product can be obtained upon amplification with 5pGALNiSTPCR and 3pGALNiSTPCR primers on genomic DNA (Figure 1). To release the plasmid from the genome and determine the integration site, genomic DNA was isolated from the transformants, cut (with SacI

for the genomic library transformants and with PstI for the cDNA library transformants), religated and the resulting ligation reaction was precipitated and used as a template for inverse PCR. This procedure reveals homologous integration at the insert site as well as the number of integrations (assuming PCR products are of different lengths) within the Candida genome. This analysis was performed on all selected transformants, ~32 % of which showed multiple integrations. The frequency of multiple integrations was very variable and depended on the batch of transformants analyzed.
The resulting PCR products from both analyses were subsequently sequenced and the sequences by compared with both public and proprietary sequence databases. In total 86 different genes could be identified, 45 of which were of unknown function.

For the CAI-4 transformants obtained with a genomic (non-directionally cloned) library, 26% of the selected clones (n=~150) contained the C. albicans autonomous replicating sequence, ARS2, and 15% of the clones contained a ribosomal RNA fragment.

For the CAI-4 transformants obtained with a cDNA library (n=~1850) a whole series of different gene fragments was found. As expected, also a number of genes involved in carbon source metabolism and nutrient uptake were identified.

Two examples of identified genes will be discussed, although as seen in Figures 16 to 70 similiar results were obtained for all of the sequences according to the invention. Clone 36 shows a galactose-induced impairment in growth, suggestive of a promoter interference or antisense effect (Figure 3B). In this clone recombination had occurred at the insert site as shown by amplification of a ~600bp gene fragment by inverse PCR. The s quence of the isolated gene fragment was 74 % identical to a S. cerevisiae S-adenosyl methionine synthetase 2 (SAM2) gene. Effects on SAM2 mRNA were

assessed by Northern blots on total RNA extracted from a non-transformed control strain and from clone 36 grown either in antisense-inducing or non-inducing media. The Northern blot was hybridised with an in vitro synthesized SAM2 RNA sense probe to detect antisense transcripts (Figure 5). An identical Northern blot was hybridised with an in vitro synthesized SAM2 antisense probe to detect SAM2 mRNA (Figure 5). Both blots were subsequently hybridized with a TEF3 DNA probe to allow normalization. As the sequence of the C. albicans SAM2 gene was not available at the time, a C. albicans genomic library in pYCp50 was prepared and E. coli transformants were screened for the full-length gene using the 600 bp SAM2 PCR fragment as a probe. A strongly hybridizing clone was identified and designated clone 36.13.1. This clone contained the complete ORF (1155 bp) of the SAM2 gene including 5' and 3' flanking regions. In the very A/T-rich 5' flanking region a putative TATA box could be identified at -27 bp. The 3' flanking region contains multiple T-rich (>10 bp) regions, elements described in yeast as necessary for transcript release (Reeder and Lang, 1997). The complete SAM2 mRNA transcript thus has a predicted length of 1.2 kb.

Clone 38 showed impaired growth in both non-inducing and inducing media (Figure 3); this is expected when integration of the library plasmid itself leads to gene suppression. Clone 38 contained a 340 bp fragment of the ribonucleotide reductase 1 (RNR1) gene. RNR1 mRNA levels were analysed by Northern blot and quantitative PCR in a non-transformed control strain and clone 38 grown in S+glucose medium. The Northern blot was hybridised successively with an actin and an RNR1 doublestranded DNA probe (Figure 6). Although the ß-actin transcript level in the control strain is lower compared to clone 38, the relative amount of RNR1 transcript is higher, indicating a reduced level of RNR1

transcript in clone 38. This result was confirmed by Taqman quantitative PCR on both control strain and clone 38 using a RNR1 fluorogenic probe. Resulting Ct values were calculated and normalised for ß-actin (Figure 6). Again RNR1 transcript levels in clone 38 were found reduced compared to the control strain.

To verify that the growth-effect was due to the interference with the identified gene and to support the spcificity of the antisense effect, single allele knock-outs were made in 6 identified genes using the URA-blaster method (Fonzi and irwin, 1993). Disruption of one allele of a gene should in theory lead to ~ 50 % reduction in gene transcript. In practice however we have observed reductions varying between 10 and 100 % of normal level. This can probably be explained by the fact that not always both copies of a gene are functional. That only a single integration at the corerct site had occurred for each of the disruption cassettes was verified by PCR and Southern blot analysis. Growth curves were measured; three disruptants showed impaired growth, suggesting that a gene required for growth or survival was targeted. Experiments to take over control of the second allele of each gene -by promoter replacement- are ongoing.

The present application describes new methods to diminish endogenous gene expression in the medically important yeast C. albicans. Our approach proved very useful for the identification of genes required for growth or survival. Technical hurdles consisted of the lack of an efficient transformation method for C. albicans (Logghe M., submitted) and the need to measure growth reproducibly on a large number of transformants in parallel. The latter was achieved with a Bioscreen Analyzer (Labsystems) which can simultaneously measure growth in 200 cultures and subsequently generate growth curves automatically. Although in principle this kind of screening could be done on plates we could not

achieve satisfactory reproducibility using plate screening.

In our genomic screen, integration of the library plasmid can happen either at the endogenous GAL1 promoter locus or, more frequently, at the locus corresponding to the plasmid insert. The latter results in a gene duplication with the first copy of the gene flanked by two convergently oriented promoters. The use of such a "collision construct" has previously been described in screening for inhibitors of transcriptional activation in mammalian cells (patent WO 97/10360; Giese K.). If RNA polymerase II complexes start from both the upstream and downstream, oppositely oriented, promoter regions, they may collide thereby preventing the formation of a full-length mRNA transcript. The second copy of the gene has no more a promoter and is probably 5' crippled as the original inserts cloned into the library have an average length of ~1.5 kb while ORFs in C. albicans have an average length of ... and we ourselves identified ORFs of (unknown) genes larger than 7 kb.

Upon integration of a plasmid into the C. albicans genome, reduced function of the protein encoded by the disrupted gene can be due to several mechanisms: 1) The first copy of the duplicated gene can be prevented from forming functional sense transcript by promoter collision or the sense transcript may be inhibited by true antisense. Indeed, although a 1.2 kb SAM2 antisense transcript could be detected in clone 36 we cannot exclude the growth defect being due to promoter interference. If an antisense transcript is formed from an intact SAM2 gene, we expect a transcript of at least 1055 bp; no transcription terminator was engineered upstream of this gene so transcription will proceed until an appropriate transcription termination recognition site is reached. The promoter region of the SAM2 gene is particularly A/T rich and contains a reversed yeast transcription terminator site at - 118

(with translation starting at +1). In yeast, transcription terminator sites are ill-defined but for a T-rich stretch with non-T residues situated appropriately to prevent slippage (Jeong et al., 1996; Reeder and Lang, 1997). If termination of transcription occurs at this theoretically predicted site, a 1.17 kb transcript would be expected, as was found. 2) If mutations were present in the original library clone, the protein encoded by the gene after homologous recombination could be non-functional. 3) Possible cis down-regulatory effects on adjacent genes could be induced upon integration of large DNA fragments at certain locations within the genome. 4) Finally, gene disruption could occur by recombination with cDNA that is not full-length at the 5′ end.

If -on the contrary- integration happens at the endogenous GAL1 promoter site, the GAL1 promoter is duplicated and antisense can be induced from this promoter. Promoter collision is not possible as the endogenous promoter of the gene is lacking at the integration site. Integration at a non-homologous site within the genome is rare. Transformation efficiencies of 0.7-3 transformants/μg have been reported upon transformation of CAI-4 with non-homologous plasmid DNA (Thompson et al., 1998). Also, integration at the URA3 locus is very unlikely as the complete URA3 gene has been removed from the CAI-4 genome.

Irrespective of the mechanism responsible for gene suppression, we could identify genes required for growth or survival by screening for transformants showing either galactose-induced or complete growth block. Furthermore, for such genome-wide screening no prior sequence information is needed and it allows discovery of possibly new critical functions. However, some genes may only be critical under conditions different from growth in minimal medium (as used in our screening) e.g. environments with high oxygen tension, high osmolarity

or high pH. However, it would be possible to screen for a growth phenotype under these conditions using our screening method. Alternatively, some genes may play critical roles only under unusual growth states or may specifically be required for adaptation to conditions encountered during infection of a host.

More than half of the ORFs we have identified as being critical for growth have a completely unknown function. Even though required for growth in C. albicans, for some genes no homologues could be found in existing databases, suggesting that they are species-specific genes. Indeed, recent genome sequencing efforts (e.g. Mycoplasma genitalium (Fraser et al., 1995), Haemophilus influenzae (Fleischmann et al, 1995)) have shown that approximately 20 % of the predicted ORFs in a microbial genome can be species-specific.

One disadvantage of the technique is that multiple library plasmids can integrate in the genome of a single C. albicans cell. When this occurs, identification of the target responsible for the growth defect becomes more difficult. Also, as shown in Schizosaccharomyces pombe (Atkins et al., 1995), RNA-mediated suppression may not be effective for certain genes, which we would miss when relying only on this technique.

Rather unexpectedly, transformation with the genomic library and subsequent screening for transformants showing reduced growth frequently yielded ARS2- and rRNA-containing clones (in 26 and 15% respectively of the transformants showing reduced growth). Previously, a study of aging yeast mother cells had shown that accumulation of extrachromosomal rDNA circles (ERCs) occurs in old cells and that these ERCs actually cause aging (Sinclair et al., 1997; Johnson et al., 1999). rDNA is present at 100-200 tandem copies on chromosome XII of S. cerevisiae and was found to accumulate to about 1000 copies in senescent cells.
One other gene we identified is a homologue of the

essential S. cerevisiae gene TRA1, a protein kinase showing highest identity to the human TRRAP gene (McMahon et al., 1998) which is an ataxia telangiectasia mutated (ATM)-related gene. Loss of ATM is a genetic defect identified in ataxia telangiectasia (Johnson et al., 1999), a disease in humans where life span is typically reduced to 40-50 years. We might thus have picked up a number of growth-inhibitory effects due to induction of aging.

The strategy presented should be applicable to all organisms for which existing techniques for "en masse" gene disruption are not easily applicable because of their diploid nature and lack of sexual cycle and might prove especially useful for other diploid imperfect yeasts.

Although the genomic strategy that we described cannot substitute for a comprehensive investigation of individual genes and pathways, it can provide a good starting point for such investigation.

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TABLE 1

Seq ID No.	Clone	Function
1	214c_cpL1	-
2	113g2	-
3	222g8	-
4	222g8(prt)	-
5	222g9	-
6	222g9_CDS_1	-
7	222g9_CDS_2	-
8	222g9_CDS_3	-
9	222g9_CDS_4	-
10	24gG	-
11	28gK	-
12	328c1	-
13	328c1(prt)	-
14	33gK	-
15	33gK(prt)	-
16	3gG	-
17	58gA	-
18	21g2	-
19	21g2(prt)	5' UTR TRA1
20	223c_cp	CFL
21	357cL	
22	357cL(prt)	RPL27
23	110c_af	
24	110c_af(prt)	SADH
25	CDC48	
26	CDC48(prt)	CDC48
27	99g3	
28	99g3(prt)	CIT
29	ESP1	
30	ESP1(prt)	ESP1
31	190g3	
32	190g3(prt)	FAL1
33	249c_af	
34	249c_af(prt)	MAA
35	485cL	
36	485cL(prt)	RPL16
37	328c3	
38	328c3(prt)	RPS21
39	83c3	
40	83c3(prt)	SHA3
41	233c_cp2	
42	233c_cp2	TPI1
43	214c_cpL1	HXT6_2
44	128g4	15S rRNA
45	135g	tRNA_Ser

Seq ID No.	Clone	Function
46	22g3	
47	22g3_CDS1	
48	22g3_CDS2	-
49	38g1	-
50	117c_af	-
51	117c_af(prt)	-
52	17g1	-
53	17g1_CDS1	-
54	17g1_CDS2	-
55	480c	-
56	480c(prt)	-
57	55g3	-
58	55g3(prt)	-
59	61gB	
60	61gB(prt)	PSP2
61	62gB	
62	62gB(prt)	-
63	80g3	
64	80g3(prt)	-
65	29g2_part1	
66	29g2_part1(prt)	EF4
67	29g2_part2_3	
68	29g2_part2(prt)	EF4
69	29g2_part3(prt)	EF4
70	226c_af2	
71	226c_af2(prt)	ADE12
72	409c5	
73	409c5(prt)	HOL1
74	40c_af	
75	40c_af(prt)	FBP
76	55g1	
77	55g1(prt)	MEG1
78	67g1	
79	67g1(prt)	RVS167
80	232c_cp	
81	360c6	
82	360c6(prt)	HXT6_1
83	98c_cp	
84	98c_cp(prt)	KGD2
85	17c_cp	
86	17c_cp(prt)	NDE1
87	60gK	
88	60gK(prt)	RAD18
89	226c_af1	
90	226c_af1(prt)	-
91	328c2	
92	328c2(prt)	-
93	498c_cp	

Seq ID No.	Clone	Function
94	498c_cp(prt)	-
95	64gB	
96	64gB(prt)	-
97	8c_cp	
98	8c_cp(prt)	-
99	15c1	
100	15c1(prt)	-
101	233c_cp1	
102	233c_cp1_CDS1	
103	233c_cp1_CDS2	-
104	35gK	
105	35gK(prt)	-
106	36g2	
107	36g2(prt)	-
108	65g	
109	65g(prt)	-
110	85g3	
111	85g3(prt)	
112	232c_cp(prt)	SAP
113	409c10	
114	409c10(prt)	-

KNOCK-OUT DATA SHEET

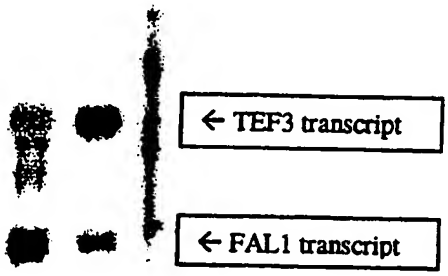
A. FAL1 single allele knock-out

Correct and single integration of FAL1 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level

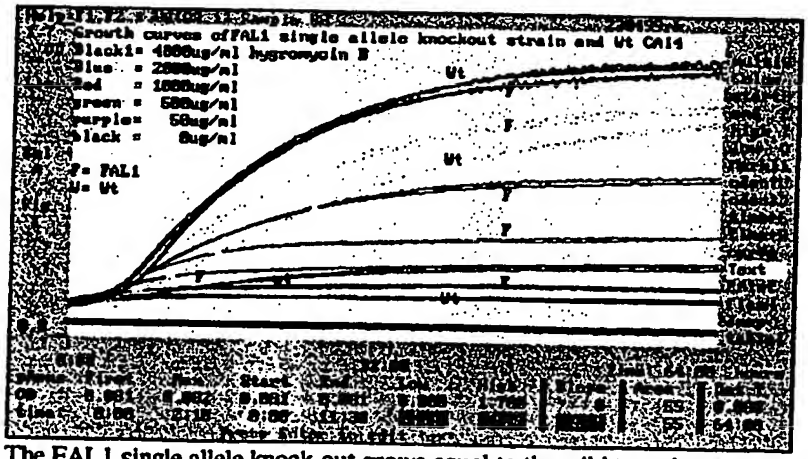
Northern blot analysis:

Lane 1: RNA MWM I (Boerhinger Mannheim)
Lane 2: WT + gal + mal + LiAc
Lane 3: FAL1 + gal + mal + LiAc
Lane 4: RNA MWM I DIG labeled (Boerhinger Mannheim)



Lower FAL1 transcript levels are observed in the FAL1 single allele knock-out strain compared to the wild type strain.

2. Growth analysis

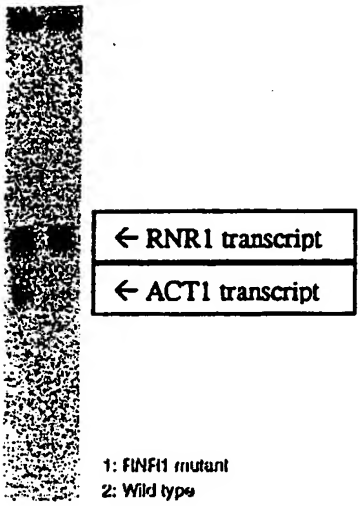


The FAL1 single allele knock-out grows equal to the wild type, however it is significantly more resistant to Hygromycin B.

B. RNR1 single allele knock-out

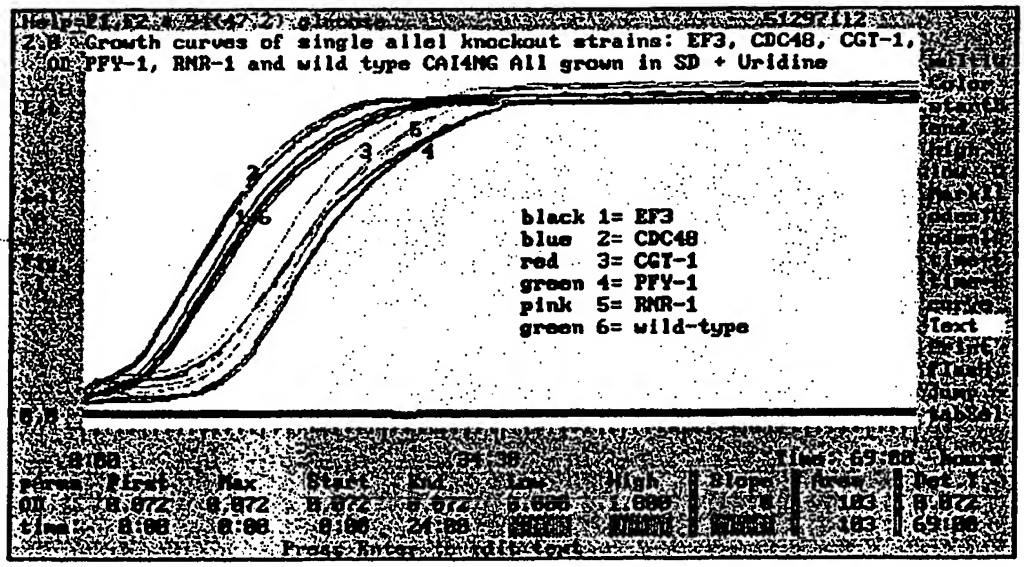
Correct and single integration of RNR1 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level
Northern blot analysis:



Lower RNR1 transcript levels are observed in the RNR1 single allele knock-out strain compared to the wild type strain. This result was confirmed by quantitative PCR (QT-PCR).

2. Growth analysis



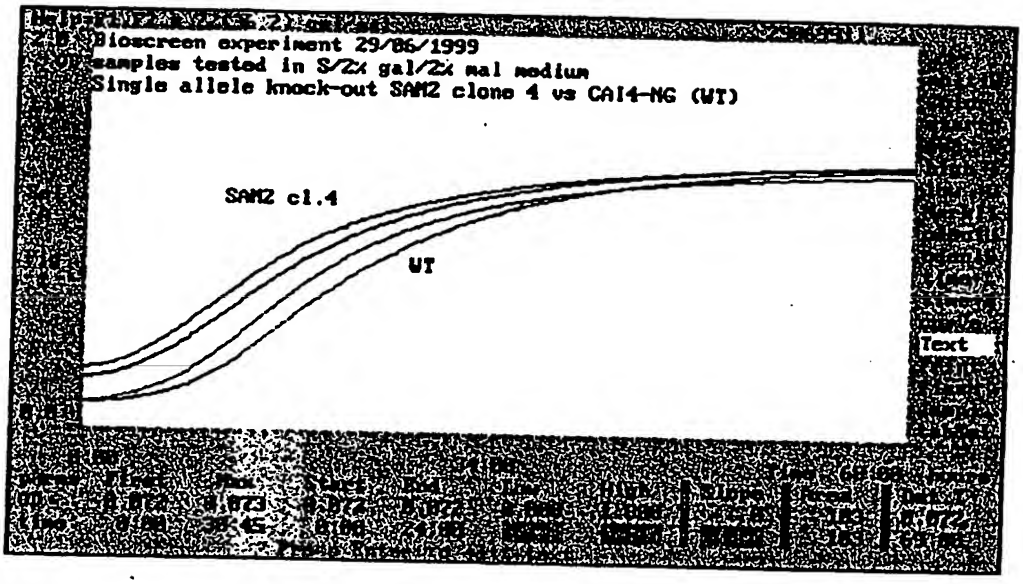
The RNR1 single allele knock-out shows an extended LAG phase compared to the wild type.

C. SAM2 single allele knock-out

Correct and single integration of SAM2 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level
Northern blot analysis:

2. Growth analysis



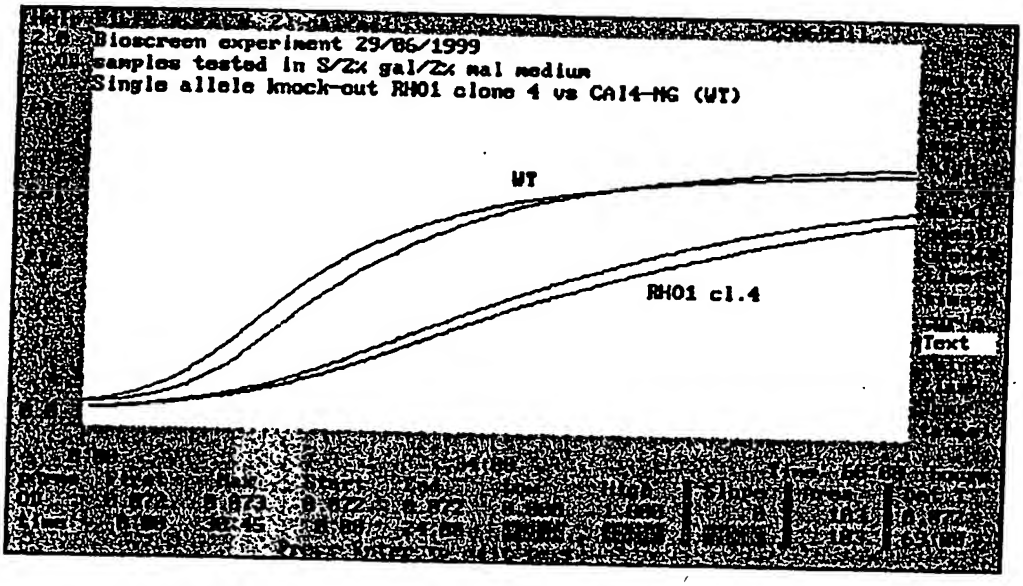
Inoculum for SAM2 was somewhat higher; at equal inocula growth of SAM2 single allele knock-out is slightly slower.

D. RHO1 single allele knock-out

Correct and single integration of RHO1 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level
Northern blot analysis:

2. Growth analysis



Growth of the RHO1 single allele knock-out is impaired compared to wild type growth.

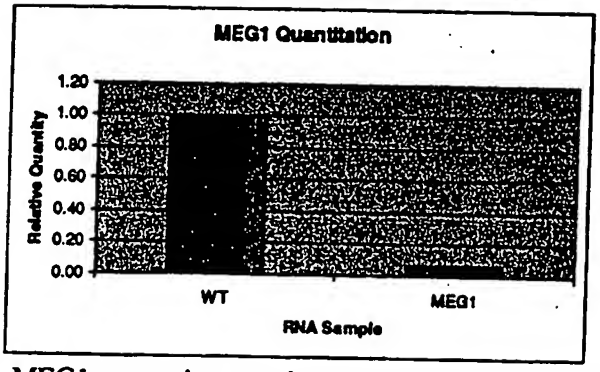
E. MEG1 single allele knock-out

Correct and single integration of MEG1 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level
QT-PCR analysis:

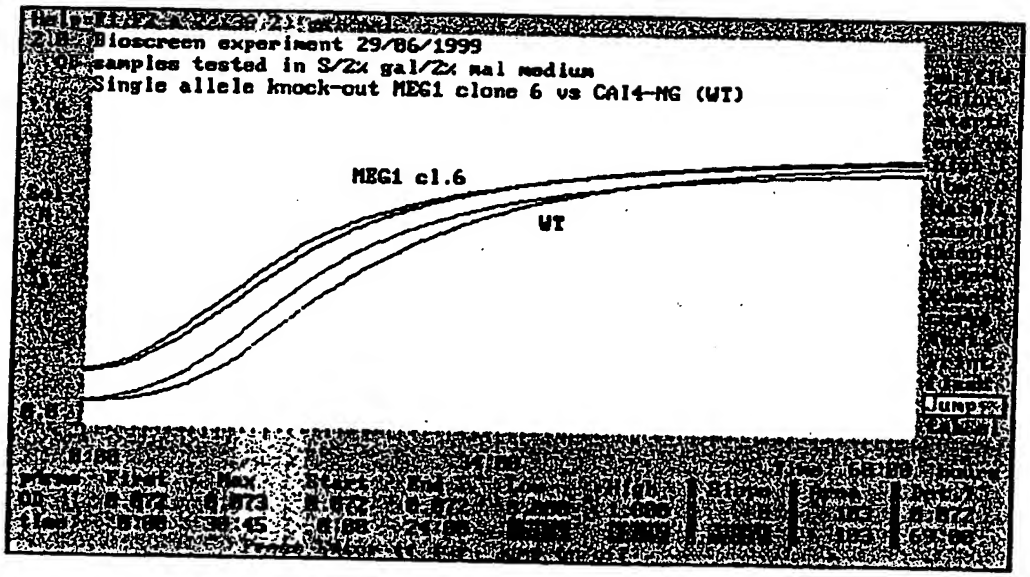
Relative quantitation for MEG1 vs. Act

	Avrg. MEG1	Avrg. ACT	dCt	ddCt	2-ddct
WT	35.79	33.49	2.29	0.00	1.00
MEG1	38.62	32.57	6.05	3.76	0.07



MEG1 expression was decreased more than 14 fold in the MEG1 single allele knock-out compared to the Wt.

2. Growth analysis



Inoculum for SAM2 was somewhat higher; at equal inocula growth of SAM2 single allele knock-out is slightly slower.

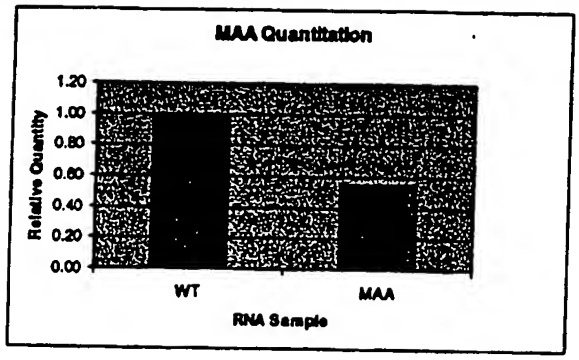
F. MAA single allele knock-out

Correct and single integration of MAA disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level
QT-PCR analysis:

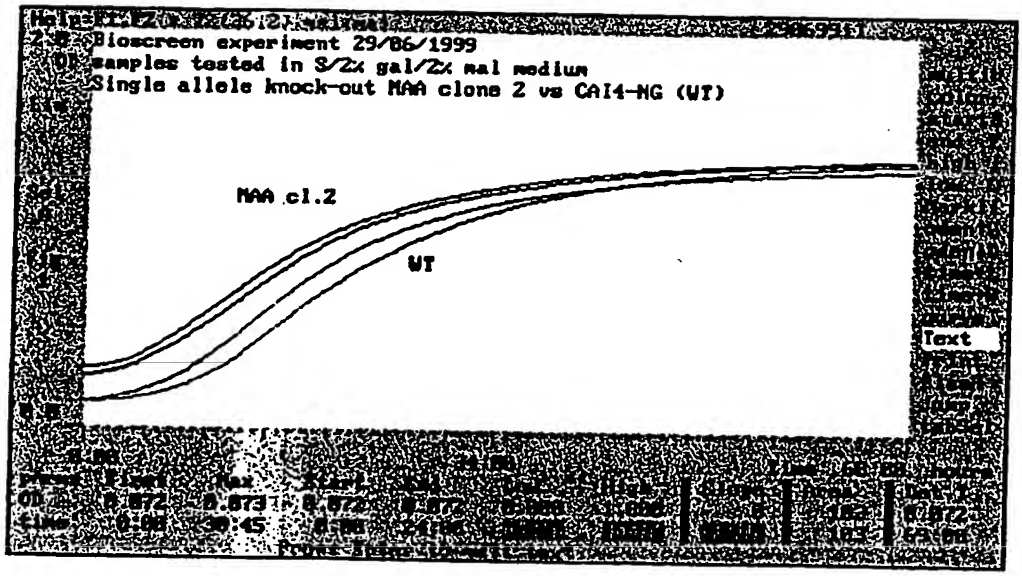
Relative quantitation for MAA vs. Act

	Avrg.MAA	Avrg. ACT	dCt	ddCt	2-ddct
WT	34.85	33.49	1.36	0.00	1.00
MAA	32.86	30.64	2.22	0.86	0.55



MAA expression was decreased two fold in the MAA knock-out compared to the Wt.

2. Growth analysis



Inoculum for MAA was somewhat higher; at equal inocula growth of MAA single allele knock-out is slightly slower.

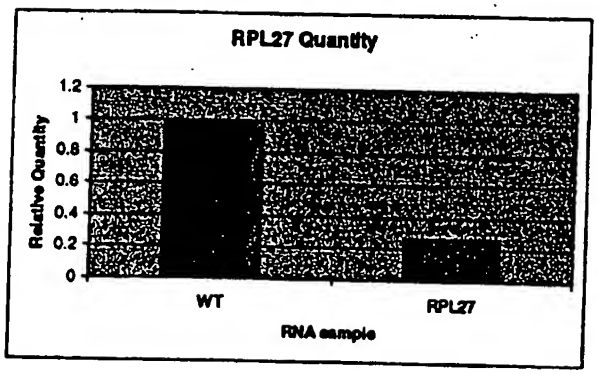
G. RPL27 single allele knock-out

Correct and single integration of RPL27 disruption cassette was confirmed by both PCR and Southern blot analysis (see support data on CD-ROM)

1. Analysis on RNA level
QT-PCR analysis:

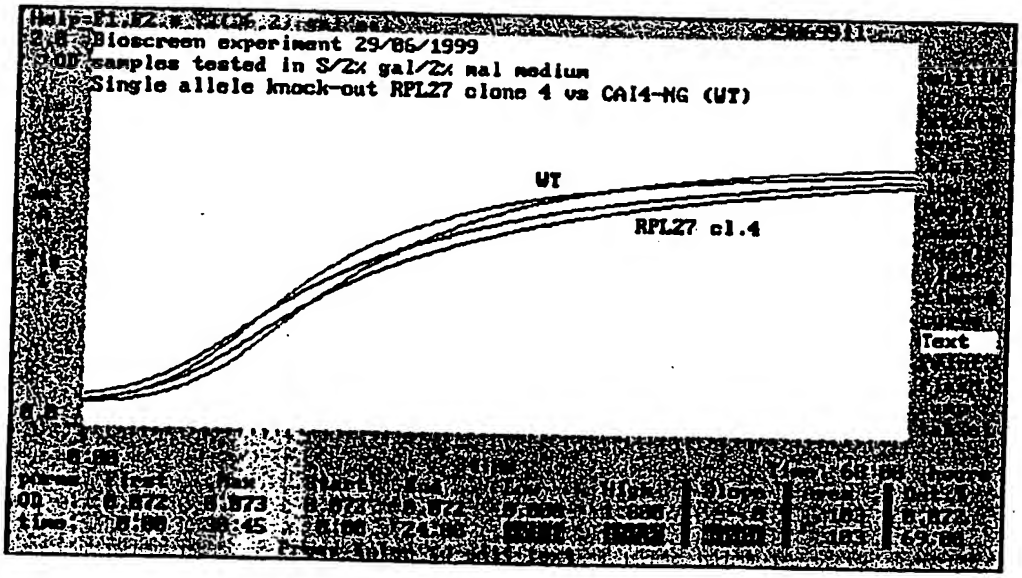
Relative quantitation for RPL27 vs. Act

	Avrg. RPL27	Avrg. ACT	dCt	ddCt	2-ddct
WT	33.01	33.49	-0.48	0.00	1
RPL27	34.37	32.98	1.39	1.87	0.27



RPL27 expression was decreased more than three fold in the RPL27 knock-out compared to the Wt.

2. Growth analysis



The RPL27 single allele knock-out grows equally to the wild type strain.

Claims

1. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast Candida albicans and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 1, 2, 3. 5, 10, 11, 12, 14, 16, 17, 18, 20, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 44, 45, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 67, 70, 72, 74, 76, 78, 80, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, 110 and 113 or the sequences of nucleotides identified in Figures 9 to 13.

2. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast Candida albicans and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 1, 2, 3, 5, 10, 11, 12, 14, 16, 17, 18, 46, 49, 50, 52, 55, 57, 59, 61, 63, 65, 87, 89, 91, 93, 95, 97, 99, 101, 104, 106, 108, and 110, or fragments or derivatives of said nucleic acid molecules.

3. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast Candida albicans and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 20, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 45, 65, 70, 72, 74, 76, 78, 80, 81, 83, 85, 113, and fragments or derivatives of said nucleic acid molecules.

4. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast Candida albicans and which nucleic acid molecule comprises any of the sequences of nucleotides of sequence ID Nos 1 and 91.

5. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast Candida albicans and which polypeptide has an amino acid sequence according to the sequence of any of Sequence ID Numbers 4, 6 to 9, 13, 15, 19, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 43, 47, 48, 51, 53, 54, 56, 58, 60, 62, 64, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 103, 105, 107, 109, 111, 112, and 114 or the sequences identified in Figures 14 and 15.

6. A nucleic acid molecule according to any one of claims 1 to 5 which is mRNA.

7. A nucleic acid molecule according to any of claims 1 to 5 which is DNA.

8. A nucleic acid molecule according to claim 7 which is cDNA.

9. A nucleic acid molecule capable of hybridising to the molecules according to any of claims 1 to 5 under high stringency conditions.

10. A nucleic acid molecule according to claim 9 which is an antisense molecule.

11. A polypeptide encoded by the nucleic acid molecule according to any of claims 1 to 8.

12. A polypeptide which is critical for survival and growth of the yeast Candida albicans having the amino acid sequences of any of Sequence ID Numbers 4, 6 to 9, 13, 15, 19, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 43, 47, 48, 51, 53, 54, 56, 58, 60, 62, 64, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 103, 105, 107, 109, 111, 112, and 114.

13. A polypeptide according to claim 12 having an amino acid sequence of any of Sequence ID Numbers 4, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 66, 68, 69, 71, 73, 75, 77, 79, 82, 84, 86 and 114.

14. A polypeptide according to claim 12 having an amino acid sequence of any of Sequence ID Nos 43 or 92.

15. An expression vector comprising a nucleic acid molecule according to claim 7 or 8.

16. An expression vector according to claim 15 which comprises an inducible promoter.

17. An expression vector according to claim 15 or 16 which comprises a sequence encoding a reporter molecule.

18. A nucleic acid molecule according to any of claims 1 to 10 for use as a medicament.

19. Use of a nucleic acid molecule according to any of claims 1 to 10 in the preparation of a medicament for treating Candida albicans associated diseases.

20. A polypeptide according to any of claims 11 to 14 for use as a medicament.

21. Use of a polypeptide according to any of claims 11 to 14 in the preparation of a medicament for treating Candida albicans associated infections.

22. A pharmaceutical composition comprising a nucleic acid molecule according to any of claims 1 to 10 or a polypeptide according to any of claims 11 to 14 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

23. A Candida albicans cell comprising an induced mutation in the DNA sequence encoding a polypeptide according to any of claims 11 to 14.

24. A method of identifying compounds which selectively modulate expression of polypeptides which are crucial for growth and survival of Candida albicans, which method comprises:

(a) contacting a compound to be tested with one or more Candida albicans cells having a mutation in a nucleic acid molecule corresponding to the sequences according to any of claims 1 to 8 which mutation results in overexpression or underexpression of said polypeptides, in addition to contacting one or more wild type Candida albicans cells with said compound,

(b) monitoring the growth and/or activity of said mutated cell compared to said wild type; wherein differential growth or activity of said one or more mutated Candida cells is indicative of selective action of said compound on a polypeptide or another polypeptide in the same or a parallel pathway.

25. A compound identifiable according to the method of claim 24.

26. A compound according to claim 25 for use as a medicament.

27. Use of a compound according to claim 25 in the preparation of a medicament for treating Candida albicans associated diseases.

28. A pharmaceutical composition comprising a

compound according to claim 24 together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

29. A method of identifying DNA sequences from a cell or organism which DNA encodes polypeptides which are critical for growth or survival of said cell or organism, which method comprises:

(a) preparing a cDNA or genomic library from said cell or organism in a suitable expression vector which vector is such that it can either integrate into the genome in said cell or that it permits transcription of antisense RNA from the nucleotide sequences in said cDNA or genomic library,

(b) selecting transformants exhibiting impaired growth and determining the nucleotide sequence of the cDNA or genomic sequence from the library included in the vector from said transformant.

30. A method according to claim 29 wherein said cell or organism is a yeast or filamentous fungi.

31. A method according to claim 29 or 30 wherein said cell or organism is any of *Saccharomyces cervisiae*, *Saccharomyces pombe* or *Candida albicans*.

32. Plasmid pGAL1PSiST-1 having the sequence of nucleotides illustrated in Figure 8.

33. Plasmid pGAL1PNiST-1 having the sequence of nucleotides illustrated in Figure 7.

34. An antibody capable of binding to a polypeptide according to any of claims 11 to 14.

35. An oligonucleotide comprising a fragment of from 10 to 50 contiguous nucleic acid sequences of a nucleic acid molecule according to any of claims 1 to 10.

36. A nucleic acid molecule encoding a polypetide which is critical for survival and growth of the yeast Candida albicans, said nucleic acid molecule comprising the sequences of any of the nucleotide sequences illustrated in Figures 9 to 13.

37. A polypeptide which is critical for survival and growth of the yeast Candida albicans, said polypeptide comprising the amino acid sequences of any of the sequences illustrated in Figures 14 or 15.

38. A method of identifying for the presence of Candida albicans in a subject, which method comprises contacting a sample to be tested with nucleic acid molecule according to claim 10 or an antibody according to claim 34, and monitoring for any hybridsation with said molecule or binding to said antibody.

39. A kit for monitoring Candida albicans infection comprising a molecule according to claim 9 or 10, or an antibody according to claim 34, and means for contacting said molecule or said antibody with a sample to be tested.

40. A nucleic acid molecule encoding a polypeptide which is critical for survival and growth of the yeast Candida albicans and which nucleic acid molecule comprises any of the sequences of nucleotides in Sequence ID Numbers 18, 21, 29, 31, 33, 44, 76, 80 and the sequences identified in Figures 9 and 13.

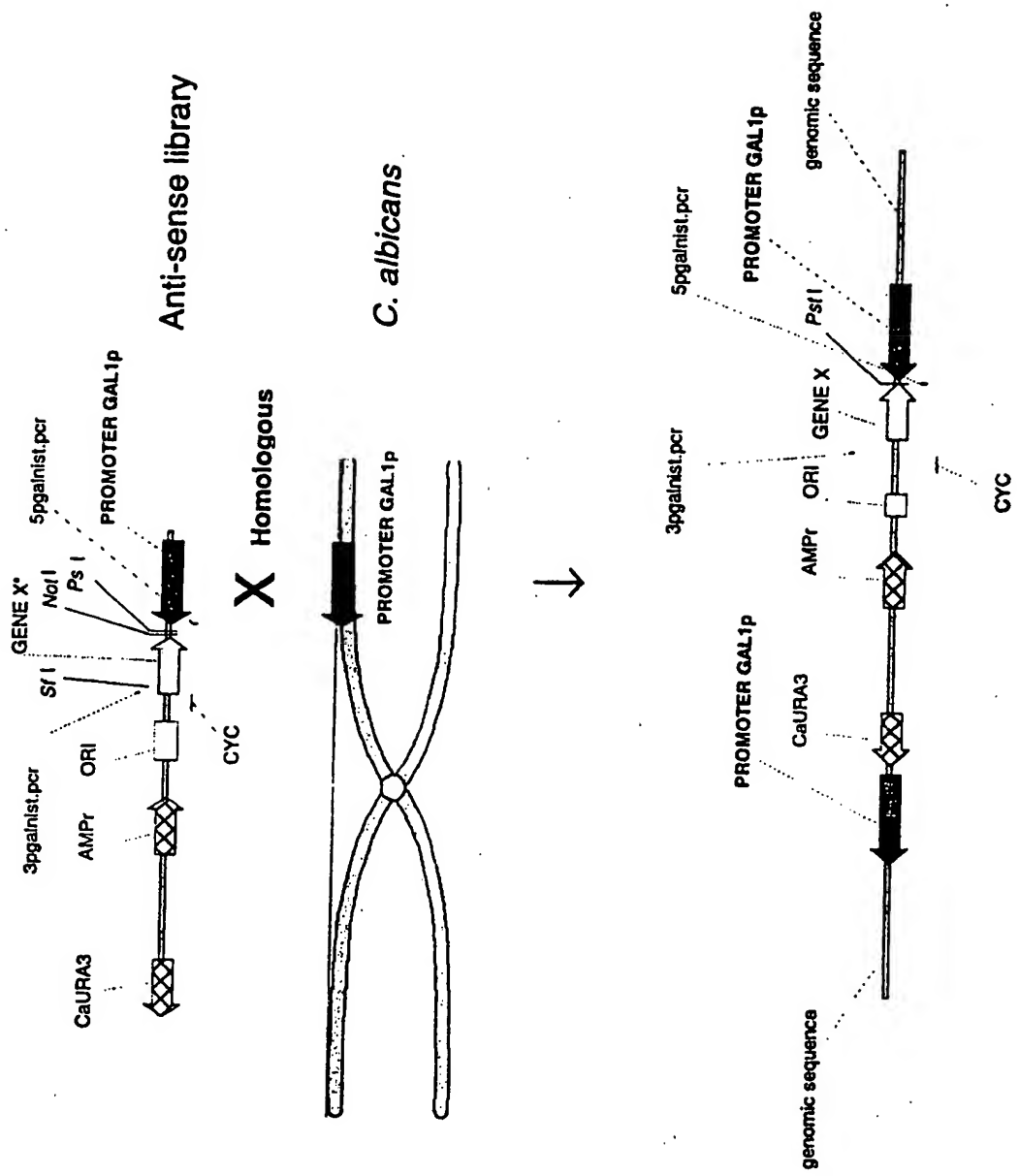

Anti-sense library
5pgalnist.pcr
PROMOTER GAL1p
GENE X'
Not I
Ps I
Sf I
CYC
3pgalnist.pcr
ORI
AMPr
CaURA3
X Homologous
C. albicans
PROMOTER GAL1p
5pgalnist.pcr
PROMOTER GAL1p
genomic sequence
Pst I
GENE X
3pgalnist.pcr
ORI
CYC
AMPr
PROMOTER GAL1p
CaURA3
genomic sequence

Figure 1A:

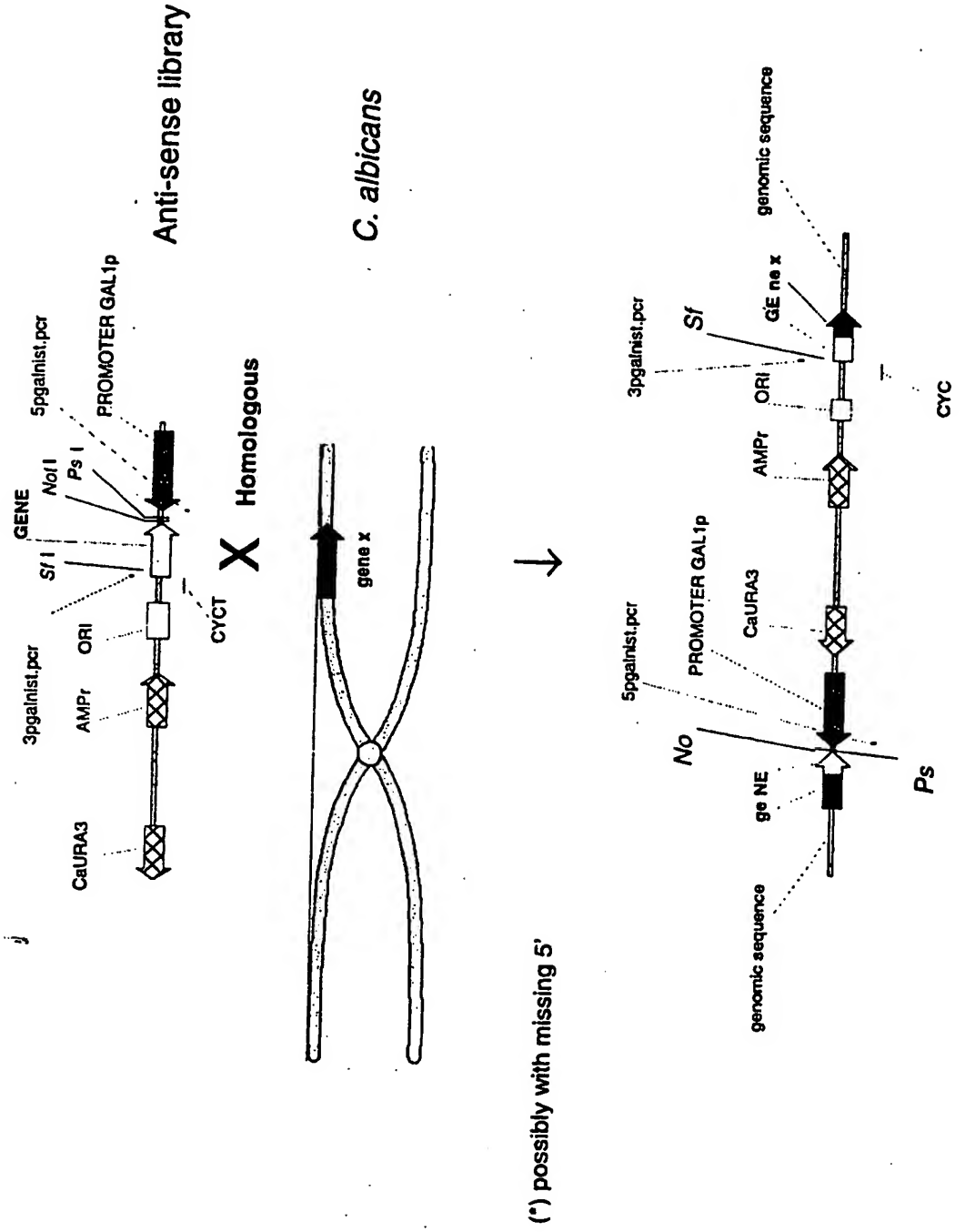

Anti-sense library
C. albicans
Homologous
5pgalnist.pcr
PROMOTER GAL1p
GENE
Not I
Ps I
Sf I
3pgalnist.pcr
ORI
AMPr
CaURA3
CYCT
gene x
(*) possibly with missing 5'
genomic sequence
GE ne x
Sf
3pgalnist.pcr
ORI
AMPr
CaURA3
PROMOTER GAL1p
5pgalnist.pcr
No
ge NE
Ps
CYC
genomic sequence

Figure 1B:

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FIG. 2(a)

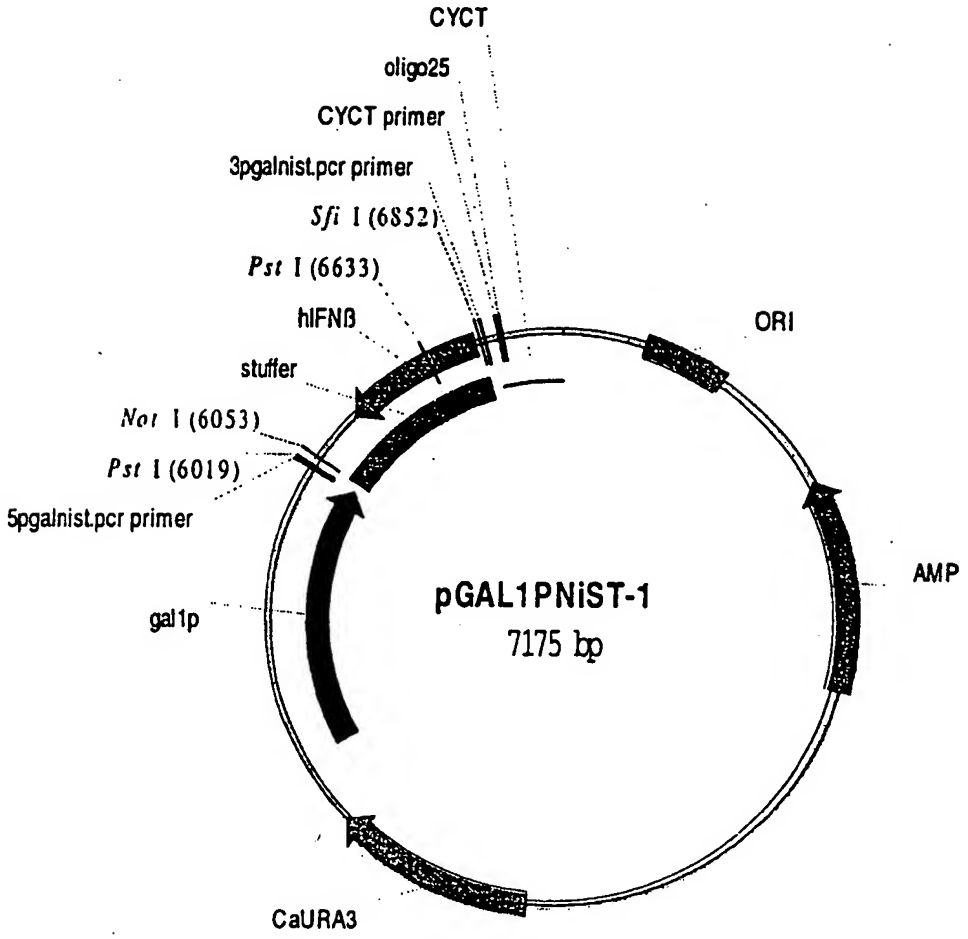
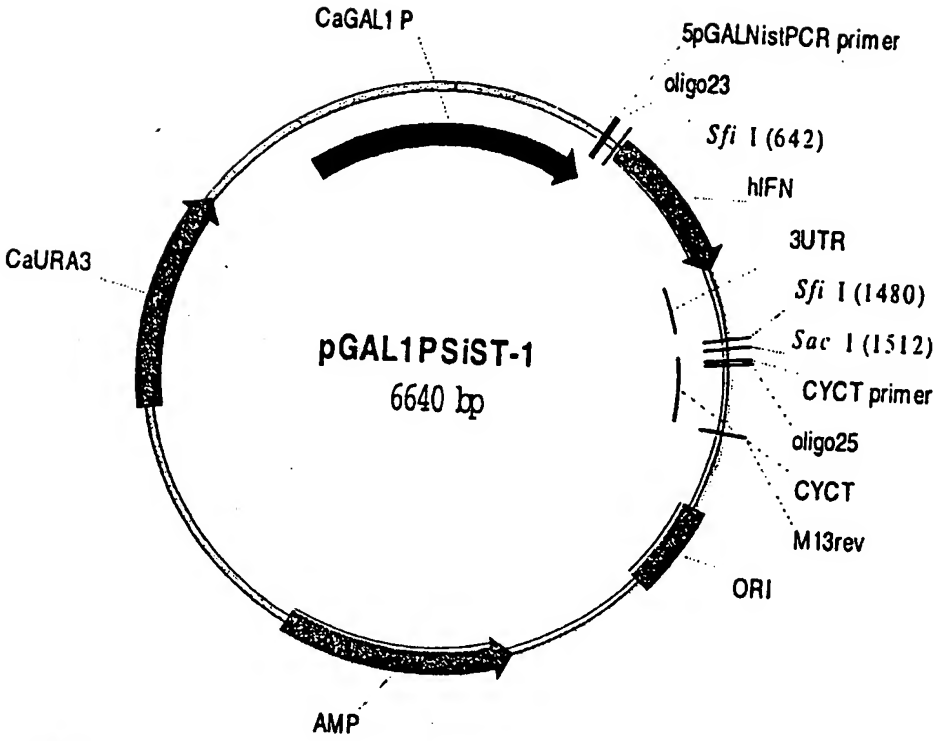

CYCT
oligo25
CYCT primer
3pgalnist.pcr primer
Sfi I (6852)
Pst I (6633)
hIFNß
stuffer
Not I (6053)
Pst I (6019)
5pgalnist.pcr primer
gal1p
CaURA3
ORI
AMP
pGAL1PNiST-1
7175 bp

FIG. 2(b)


CaGAL1 P
5pGALNistPCR primer
oligo23
Sfi I (642)
hIFN
3UTR
Sfi I (1480)
Sac I (1512)
CYCT primer
oligo25
CYCT
M13rev
ORI
AMP
CaURA3
pGAL1PSiST-1
6640 bp

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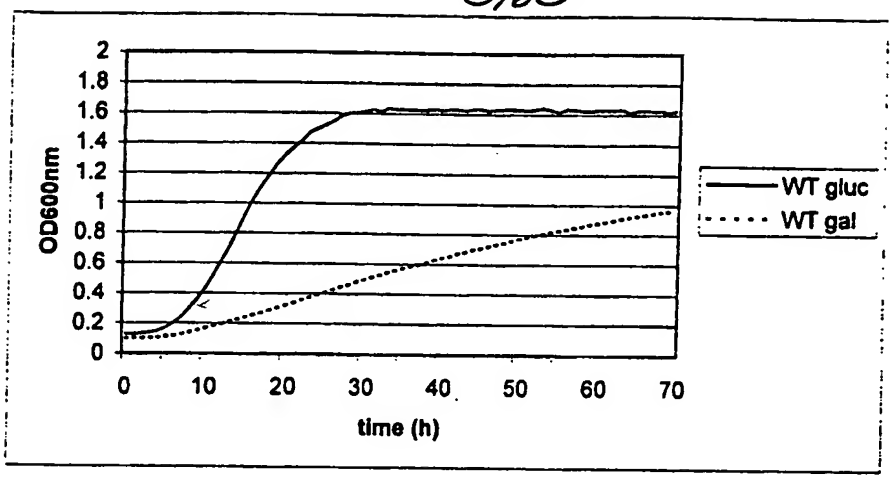
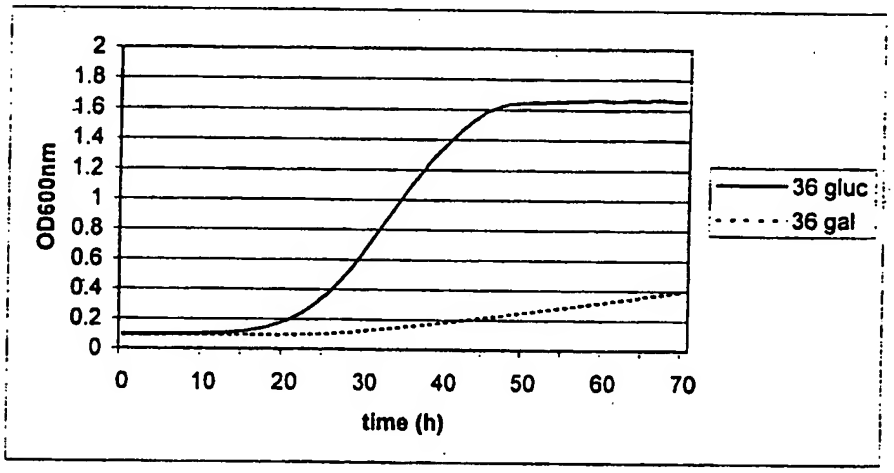

OD600nm
time (h)
WT gluc
WT gal


OD600nm
time (h)
36 gluc
36 gal

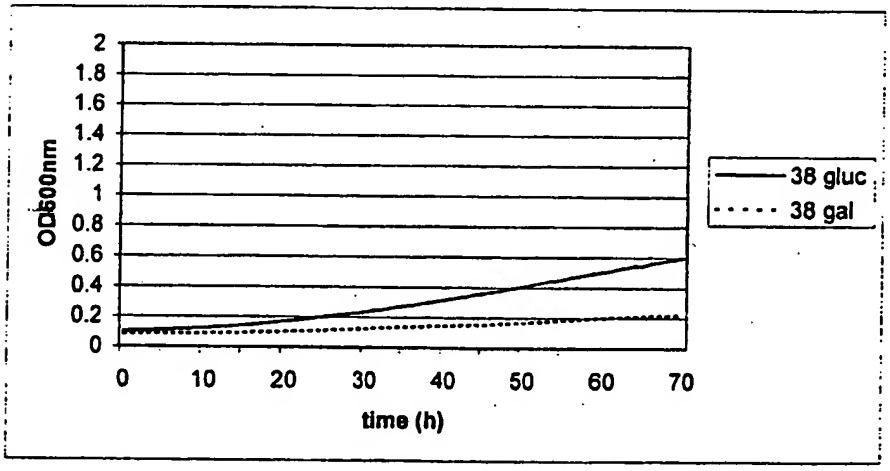
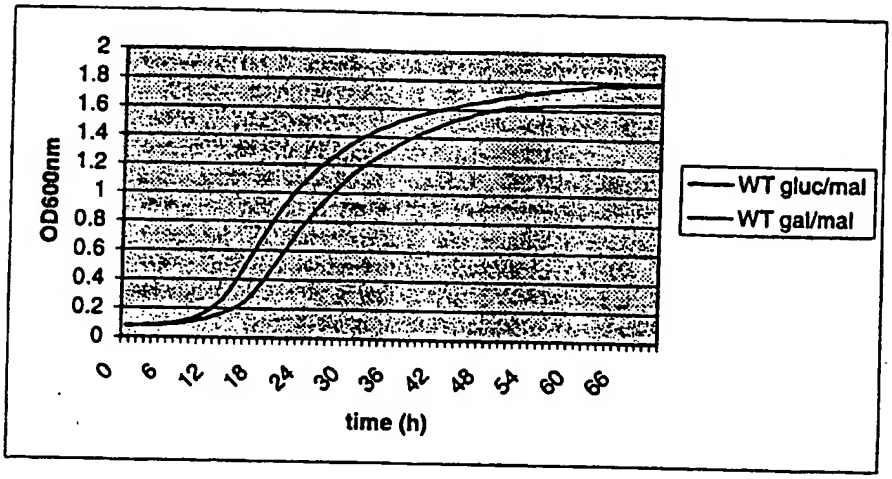
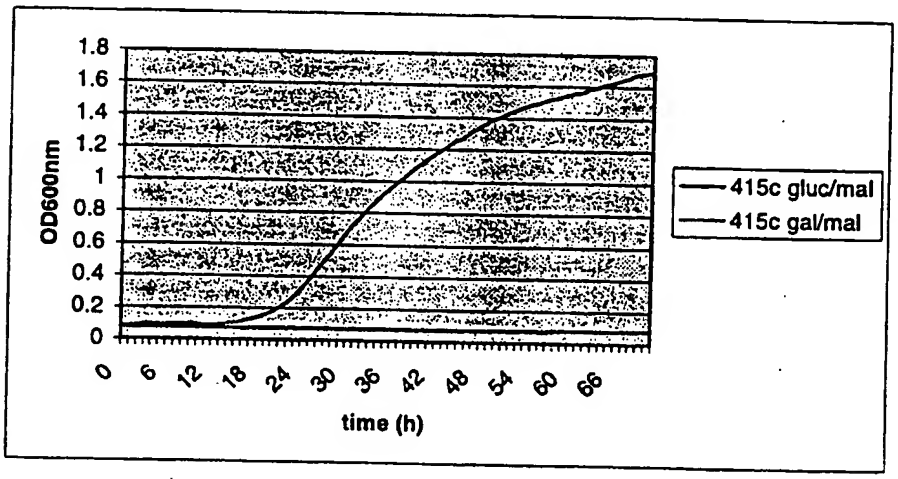

OD600nm
time (h)
38 gluc
38 gal

FIG. 3.





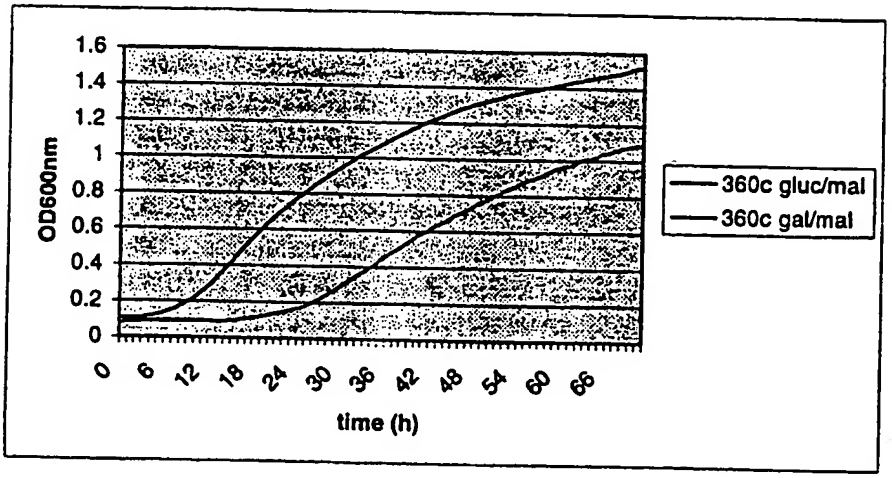


FIG. 3 (CONTINUED)

FIG. 4.

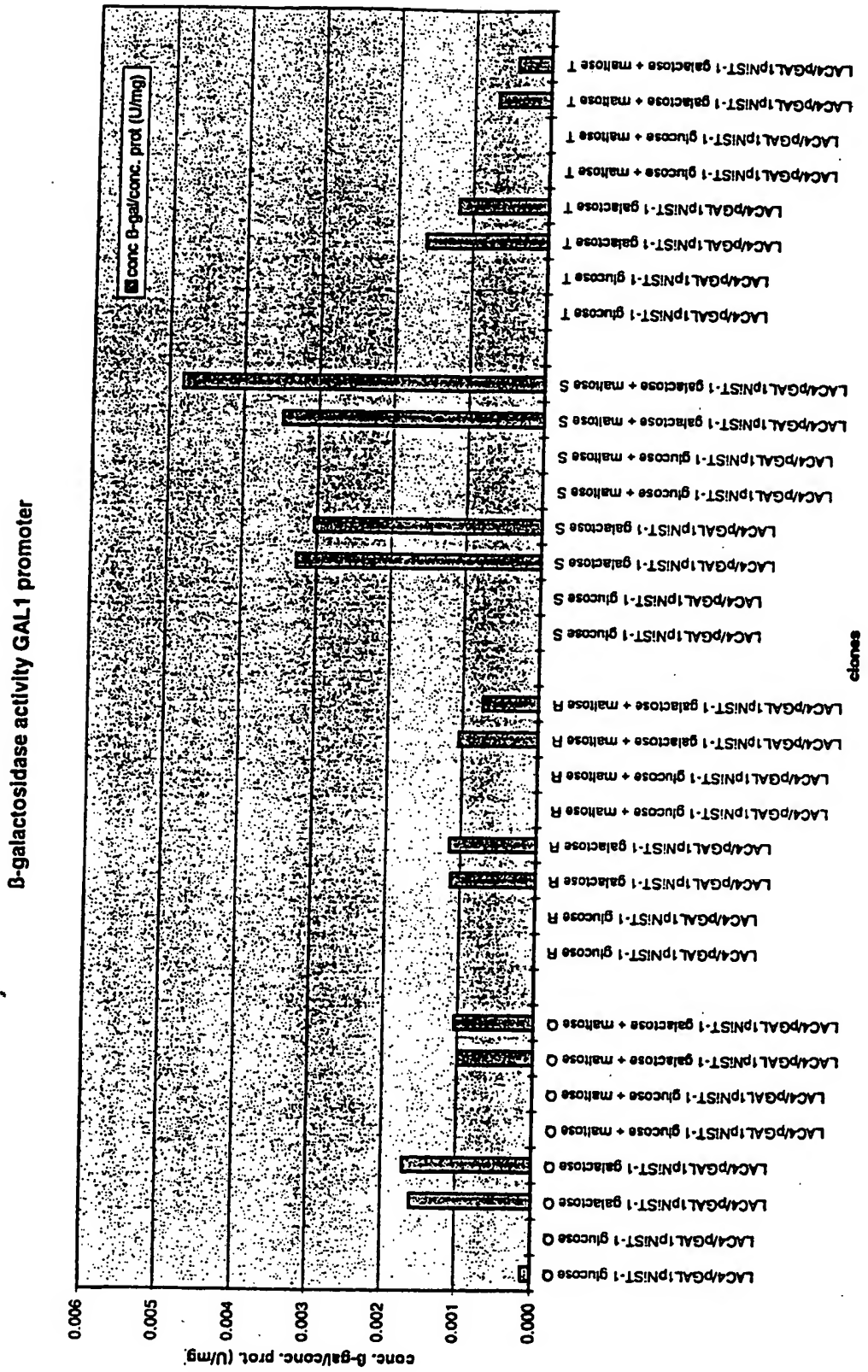

ß-galactosidase activity GAL1 promoter
conc. ß-gal/conc. prot. (U/mg)
0.006
0.005
0.004
0.003
0.002
0.001
0.000
conc ß-gal/conc. prot (U/mg)
clones
LAC4/pGAL1pNIST-1 glucose O
LAC4/pGAL1pNIST-1 glucose O
LAC4/pGAL1pNIST-1 galactose O
LAC4/pGAL1pNIST-1 galactose O
LAC4/pGAL1pNIST-1 glucose + maltose O
LAC4/pGAL1pNIST-1 glucose + maltose O
LAC4/pGAL1pNIST-1 galactose + maltose O
LAC4/pGAL1pNIST-1 galactose + maltose O
LAC4/pGAL1pNIST-1 glucose R
LAC4/pGAL1pNIST-1 glucose R
LAC4/pGAL1pNIST-1 galactose R
LAC4/pGAL1pNIST-1 galactose R
LAC4/pGAL1pNIST-1 glucose + maltose R
LAC4/pGAL1pNIST-1 glucose + maltose R
LAC4/pGAL1pNIST-1 galactose + maltose R
LAC4/pGAL1pNIST-1 galactose + maltose R
LAC4/pGAL1pNIST-1 glucose S
LAC4/pGAL1pNIST-1 glucose S
LAC4/pGAL1pNIST-1 galactose S
LAC4/pGAL1pNIST-1 galactose S
LAC4/pGAL1pNIST-1 glucose + maltose S
LAC4/pGAL1pNIST-1 glucose + maltose S
LAC4/pGAL1pNIST-1 galactose + maltose S
LAC4/pGAL1pNIST-1 galactose + maltose S
LAC4/pGAL1pNIST-1 glucose T
LAC4/pGAL1pNIST-1 glucose T
LAC4/pGAL1pNIST-1 galactose T
LAC4/pGAL1pNIST-1 galactose T
LAC4/pGAL1pNIST-1 glucose + maltose T
LAC4/pGAL1pNIST-1 glucose + maltose T
LAC4/pGAL1pNIST-1 galactose + maltose T
LAC4/pGAL1pNIST-1 galactose + maltose T

Figure 5:

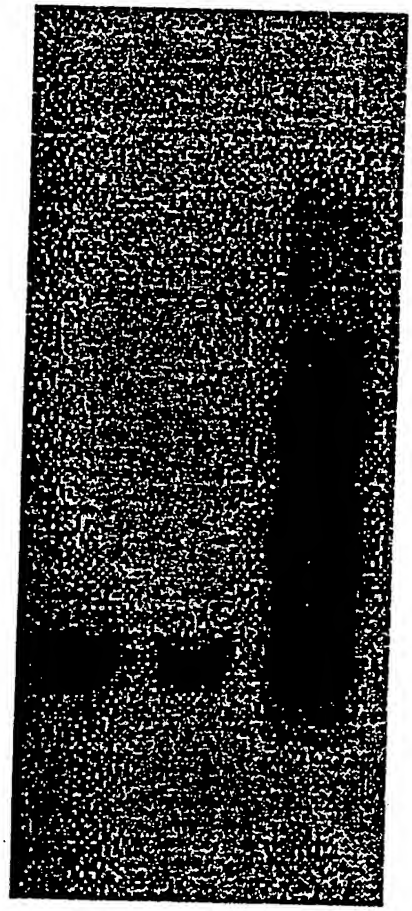


Figure 6A

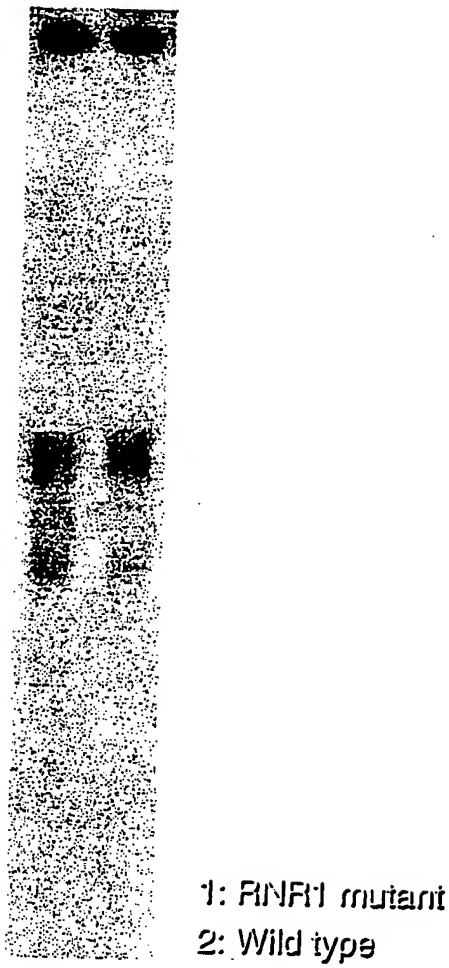


Figure 6B

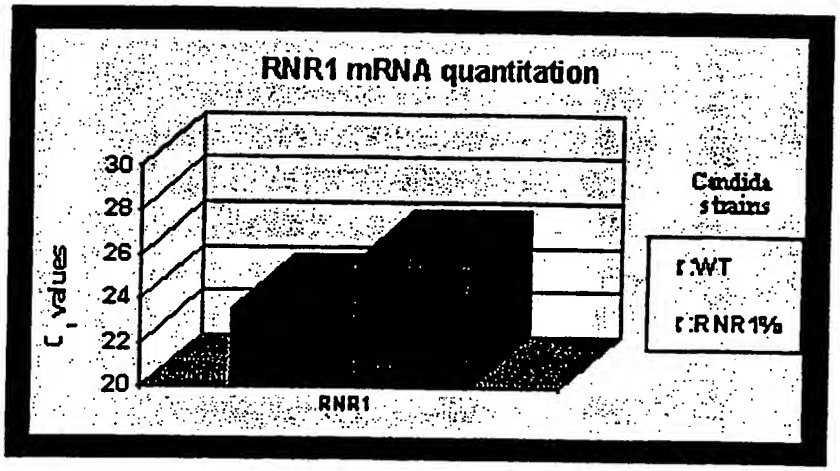

RNR1 mRNA quantitation
30
28
26
24
22
20
C_t values
RNR1
Candida strains
r:WT
r:RNR1%

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FIG. 7.

HindIII

```
  1 AGCTTGAGTA TTCTATAGTG TCACCTAAAT AGCTTGGCGT AATCATGGTC
    TCGAACTCAT AAGATATCAC AGTGGATTTA TCGAACCGCA TTAGTACCAG

 51 ATAGCTGTTT CCTGTGTGAA ATTGTTATCC GCTCACAATT CCACACAACA
    TATCGACAAA GGACACACTT TAACAATAGG CGAGTGTTAA GGTGTGTTGT

101 TACGAGCCGG AAGCATAAAG TGTAAAGCCT GGGGTGCCTA ATGAGTGAGC
    ATGCTCGGCC TTCGTATTTC ACATTTCGGA CCCCACGGAT TACTCACTCG

151 TAACTCACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA
    ATTGAGTGTA ATTAACGCAA CGCGAGTGAC GGGCGAAAGG TCAGCCCTTT

201 CCTGTCGTGC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG
    GGACAGCACG GTCGACGTAA TTACTTAGCC GGTTGCGCGC CCCTCTCCGC

251 GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT CGCTCACTGA CTCGCTGCGC
    CAAACGCATA ACCCGCGAGA AGGCGAAGGA GCGAGTGACT GAGCGACGCG

301 TCGGTCGTTC GGCTGCGGCG AGCGGTATCA GCTCACTCAA AGGCGGTAAT
    AGCCAGCAAG CCGACGCCGC TCGCCATAGT CGAGTGAGTT TCCGCCATTA

351 ACGGTTATCC ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA
    TGCCAATAGG TGTCTTAGTC CCCTATTGCG TCCTTTCTTG TACACTCGTT

401 AAGGCCAGCA AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT
    TTCCGGTCGT TTTCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAAA

451 TTCCATAGGC TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG
    AAGGTATCCG AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC

501 TCAGAGGTGG CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC
    AGTCTCCACC GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG

551 CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA
    GACCTTCGAG GGAGCACGCG AGAGGACAAG GCTGGGACGG CGAATGGCCT

601 TACCTGTCCG CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC
    ATGGACAGGC GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG

651 ACGCTGTAGG TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT
    TGCGACATCC ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA
```

ApaLI

```
701 GTGTGCACGA ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC
    CACACGTGCT TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG

751 TATCGTCTTG AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC
    ATAGCAGAAC TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG

801 AGCCACTGGT AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG
    TCGGTGACCA TTGTCCTAAT CGTCTCGCTC CATACATCCG CCACGATGTC

851 AGTTCTTGAA GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT
    TCAAGAACTT CACCACCGGA TTGATGCCGA TGTGATCTTC CTGTCATAAA

901 GGTATCTGCG CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG
    CCATAGACGC GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC
```

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FIG. 7. (CONTINUED)

```
 951  CTCTTGATCC GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT
      GAGAACTAGG CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA
 .....
1001  GCAAGCAGCA GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG
      CGTTCGTCGT CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC
 .....
1051  ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG
      TAGAAAAGAT GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC
 .....
1101  GATTTTGGTC ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA
      CTAAAACCAG TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAATT
 .....
1151  ATTAAAAATG AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG
      TAATTTTTAC TTCAAAATTT AGTTAGATTT CATATATACT CATTTGAACC
 .....
1201  TCTGACAGTT ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG
      AGACTGTCAA TGGTTACGAA TTAGTCACTC CGTGGATAGA GTCGCTAGAC
 .....
1251  TCTATTTCGT TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA
      AGATAAAGCA AGTAGGTATC AACGGACTGA GGGGCAGCAC ATCTATTGAT
 .....
1301  CGATACGGGA GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA
      GCTATGCCCT CCCGAATGGT AGACCGGGGT CACGACGTTA CTATGGCGCT
 .....
1351  GACCCACGCT CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG
      CTGGGTGCGA GTGGCCGAGG TCTAAATAGT CGTTATTTGG TCGGTCGGCC
 .....
1401  AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT
      TTCCCGGCTC GCGTCTTCAC CAGGACGTTG AAATAGGCGG AGGTAGGTCA
 .....
1451  CTATTAATTG TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT
      GATAATTAAC AACGGCCCTT CGATCTCATT CATCAAGCGG TCAATTATCA
 .....
1501  TTGCGCAACG TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC
      AACGCGTTGC AACAACGGTA ACGATGTCCG TAGCACCACA GTGCGAGCAG
 .....
1551  GTTTGGTATG GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA
      CAAACCATAC CGAAGTAAGT CGAGGCCAAG GGTTGCTAGT TCCGCTCAAT
 .....
1601  CATGATCCCC CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG
      GTACTAGGGG GTACAACACG TTTTTTCGCC AATCGAGGAA GCCAGGAGGC
 .....
1651  ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC
      TAGCAACAGT CTTCATTCAA CCGGCGTCAC AATAGTGAGT ACCAATACCG
 .....
1701  AGCACTGCAT AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG
      TCGTGACGTA TTAAGAGAAT GACAGTACGG TAGGCATTCT ACGAAAAGAC
 .....
1751  TGACTGGTGA GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA
      ACTGACCACT CATGAGTTGG TTCAGTAAGA CTCTTATCAC ATACGCCGCT
 .....
1801  CCGAGTTGCT CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG
      GGCTCAACGA GAACGGGCCG CAGTTATGCC CTATTATGGC GCGGTGTATC
 .....
1851  CAGAACTTTA AAAGTGCTCA TCATTGGAAA ACGTTCTTCG GGGCGAAAAC
      GTCTTGAAAT TTTCACGAGT AGTAACCTTT TGCAAGAAGC CCCGCTTTTG
 .....
```

FIG. 7. (CONTINUED) 13/63

ApaLI

1901 TCTCAAGGAT CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT
AGAGTTCCTA GAATGGCGAC AACTCTAGGT CAAGCTACAT TGGGTGAGCA

ApaLI

1951 GCACCCAACT GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG
CGTGGGTTGA CTAGAAGTCG TAGAAAATGA AAGTGGTCGC AAAGACCCAC

2001 AGCAAAAACA GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC
TCGTTTTTGT CCTTCCGTTT TACGGCGTTT TTTCCCTTAT TCCCGCTGTG

2051 GGAAATGTTG AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT
CCTTTACAAC TTATGAGTAT GAGAAGGAAA AAGTTATAAT AACTTCGTAA

2101 TATCAGGGTT ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA
ATAGTCCCAA TAACAGAGTA CTCGCCTATG TATAAACTTA CATAAATCTT

2151 AAATAAACAA ATAGGGGTTC CGCGCACATT TCCCCGAAAA GTGCCACCTG
TTTATTTGTT TATCCCCAAG GCGCGTGTAA AGGGGCTTTT CACGGTGGAC

2201 ACGTCTAAGA AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT
TGCAGATTCT TTGGTAATAA TAGTACTGTA ATTGGATATT TTTATCCGCA

2251 ATCACGAGGC CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT
TAGTGCTCCG GGAAAGCAGA GCGCGCAAAG CCACTACTGC CACTTTTGGA

2301 CTGACACATG CAGCTCCCGG AGACGGTCAC AGCTTGTCTG TAAGCGGATG
GACTGTGTAC GTCGAGGGCC TCTGCCAGTG TCGAACAGAC ATTCGCCTAC

2351 CCGGGAGCAG ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT
GGCCCTCGTC TGTTCGGGCA GTCCCGCGCA GTCGCCCACA ACCGCCCACA

ApaLI

2401 CGGGGCTGGC TTAACTATGC GGCATCAGAG CAGATTGTAC TGAGAGTGCA
GCCCCGACCG AATTGATACG CCGTAGTCTC GTCTAACATG ACTCTCACGT

ApaLI

2451 CCATATGCGG TGTGAAATAC CGCACAGATG CGTAAGGAGA AAATACCGCA
GGTATACGCC ACACTTTATG GCGTGTCTAC GCATTCCTCT TTTATGGCGT

2501 TCAGGCGAAA TTGTAAACGT TAATATTTTG TTAAAATTCG CGTTAAATAT
AGTCCGCTTT AACATTTGCA ATTATAAAAC AATTTTAAGC GCAATTTATA

2551 TTGTTAAATC AGCTCATTTT TTAACCAATA GGCCGAAATC GGCAAAATCC
AACAATTTAG TCGAGTAAAA AATTGGTTAT CCGGCTTTAG CCGTTTTAGG

2601 CTTATAAATC AAAAGAATAG ACCGAGATAG GGTTGAGTGT TGTTCCAGTT
GAATATTTAG TTTTCTTATC TGGCTCTATC CCAACTCACA ACAAGGTCAA

2651 TGGAACAAGA GTCCACTATT AAAGAACGTG GACTCCAACG TCAAAGGGCG
ACCTTGTTCT CAGGTGATAA TTTCTTGCAC CTGAGGTTGC AGTTTCCCGC

2701 AAAAACCGTC TATCAGGGCG ATGGCCCACT ACGTGAACCA TCACCCAAAT
TTTTTGGCAG ATAGTCCCGC TACCGGGTGA TGCACTTGGT AGTGGGTTTA

2751 CAAGTTTTTT GCGGTCGAGG TGCCGTAAAG CTCTAAATCG GAACCCTAAA
GTTCAAAAAA CGCCAGCTCC ACGGCATTTC GAGATTTAGC CTTGGGATTT

FIG. 7. (CONTINUED)

```
2801  GGGAGCCCCC GATTTAGAGC TTGACGGGGA AAGCCGGCGA ACGTGGCGAG
      CCCTCGGGGG CTAAATCTCG AACTGCCCCT TTCGGCCGCT TGCACCGCTC
.....
2851  AAAGGAAGGG AAGAAAGCGA AAGGAGCGGG CGCTAGGGCG CTGGCAAGTG
      TTTCCTTCCC TTCTTTCGCT TTCCTCGCCC GCGATCCCGC GACCGTTCAC
.....
2901  TAGCGGTCAC GCTGCGCGTA ACCACCACAC CCGCCGCGCT TAATGCGCCG
      ATCGCCAGTG CGACGCGCAT TGGTGGTGTG GGCGGCGCGA ATTACGCGGC
.....
2951  CTACAGGGCG CGTCCATTCG CCATTCAGGC TGCGCAACTG TTGGGAAGGG
      GATGTCCCGC GCAGGTAAGC GGTAAGTCCG ACGCGTTGAC AACCCTTCCC
.....
3001  CGATCGGTGC GGGCCTCTTC GCTATTACGC CAGCTGGCGA AAGGGGGATG
      GCTAGCCACG CCCGGAGAAG CGATAATGCG GTCGACCGCT TTCCCCCTAC
.....
3051  TGCTGCAAGG CGATTAAGTT GGGTAACGCC AGGGTTTTCC CAGTCACGAC
      ACGACGTTCC GCTAATTCAA CCCATTGCGG TCCCAAAAGG GTCAGTGCTG
.....
3101  GTTGTAAAAC GACGGCCAGT GAATTGTAAT ACGACTCACT ATAGGGCGAA
      CAACATTTTG CTGCCGGTCA CTTAACATTA TGCTGAGTGA TATCCCGCTT
.....
3151  TTGGTTTTCC AATGATGAGC ACTTTTAAAG TTCTGCTATG TGGCGCGGTA
      AACCAAAAGG TTACTACTCG TGAAAATTTC AAGACGATAC ACCGCGCCAT
.....
3201  TTATCCCGTG TTGACGCCGG GCAAGAGCAA CTCGGTCGCC GCATACACTA
      AATAGGGCAC AACTGCGGCC CGTTCTCGTT GAGCCAGCGG CGTATGTGAT
.....
3251  TTCTCAGAAT GACTTGGTTG AGTACTAATA GGAATTGATT TGGATGGTAT
      AAGAGTCTTA CTGAACCAAC TCATGATTAT CCTTAACTAA ACCTACCATA
.....
3301  AAACGGAAAC AAAAAAAAGA GCTGGTACTA CTTTCTTTAA AATTATTTTA
      TTTGCCTTTG TTTTTTTTCT CGACCATGAT GAAAGAAATT TTAATAAAAT
.....
3351  TTATTTGATT TTATTTAATA GTATATATTA TATTTTGAAC GTAGATTATT
      AATAAACTAA AATAAATTAT CATATATAAT ATAAAACTTG CATCTAATAA
.....
3401  TTGTTGAAAG TTGCTGTAGT GCCATTGATT CGTAACACTA ATTCTGTATT
      AACAACTTTC AACGACATCA CGGTAACTAA GCATTGTGAT TAAGACATAA
.....
3451  AGTCATTCCT CTTGTTTGAT AGTATCCAAA AAAACGGCTA TTTTTTTGCA
      TCAGTAAGGA GAACAAACTA TCATAGGTTT TTTTGCCGAT AAAAAAACGT
.....
3501  ATCTTATTTC CTGCATATTA TACAGATAAC ATAATGAAAG AAAAAATCTT
      TAGAATAAAG GACGTATAAT ATGTCTATTG TATTACTTTC TTTTTTAGAA
.....
3551  TTTTTTTGTT CTTCAATGAT GATTTCAACC ATTCTTTTAA ACATTGATCA
      AAAAAAACAA GAAGTTACTA CTAAAGTTGG TAAGAAAATT TGTAACTAGT
.....
3601  ATTCCTGAGC AACAACCCCA TACACACTGG TTTATATACC GCCCCTTTTA
      TAAGGACTCG TTGTTGGGGT ATGTGTGACC AAATATATGG CGGGGAAAAT
.....
3651  CAGTTGAAGA AAGAAATAGA AATAGAAATA GCAAACAAAA GATATGACAG
      GTCAACTTCT TTCTTTATCT TTATCTTTAT CGTTTGTTTT CTATACTGTC
.....
3701  TCAACACTAA GACCTATAGT GAGAGAGCAG AAACTCATGC CTCACCAGTA
      AGTTGTGATT CTGGATATCA CTCTCTCGTC TTTGAGTACG GAGTGGTCAT
.....
3751  GCACAGCGAT TATTTCGATT AATGGAACTG AAGAAAACCA ATTTATGTGC
      CGTGTCGCTA ATAAAGCTAA TTACCTTGAC TTCTTTTGGT TAAATACACG
.....
```

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FIG. 7. (CONTINUED)

EcoRI

```
3801  ATCAATTGAC GTTGATACCA CTAAGGAATT CCTTGAATTA ATTGATAAAT
      TAGTTAACTG CAACTATGGT GATTCCTTAA GGAACTTAAT TAACTATTTA
3851  TAGGTCCTTA TGTATGCTTA ATCAAGACTC ATATTGATAT AATCAATGAT
      ATCCAGGAAT ACATACGAAT TAGTTCTGAG TATAACTATA TTAGTTACTA
3901  TTTTCCTATG AATCCACTAT TGAACCATTA TTAGAACTTT CACGTAAACA
      AAAAGGATAC TTAGGTGATA ACTTGGTAAT AATCTTGAAA GTGCATTTGT
3951  TCAATTTATG ATTTTTGAAG ATAGAAAATT TGCTGATATT GGTAATACCG
      AGTTAAATAC TAAAAACTTC TATCTTTTAA ACGACTATAA CCATTATGGC
4001  TAAAGAAACA ATATATTGGT GGAGTTTATA AAATTAGTAG TTGGGCAGAT
      ATTTCTTTGT TATATAACCA CCTCAAATAT TTTAATCATC AACCCGTCTA
4051  ATTACCAATG CTCATGGTGT CACTGGGAAT GGAGTGGTTG AAGGATTAAA
      TAATGGTTAC GAGTACCACA GTGACCCTTA CCTCACCAAC TTCCTAATTT
4101  ACAGGGAGCT AAAGAAACCA CCACCAACCA AGAGCCAAGA GGGTTATTGA
      TGTCCCTCGA TTTCTTTGGT GGTGGTTGGT TCTCGGTTCT CCCAATAACT
4151  TGTTAGCTGA ATTATCATCA GTGGGATCAT TAGCATATGG AGAATATTCT
      ACAATCGACT TAATAGTAGT CACCCTAGTA ATCGTATACC TCTTATAAGA
4201  CAAAAAACTG TTGAAATTGC TAAATCCGAT AAGGAATTTG TTATTGGATT
      GTTTTTTGAC AACTTTAACG ATTTAGGCTA TTCCTTAAAC AATAACCTAA
4251  TATTGCCCAA CGTGATATGG GTGGCCAAGA AGAAGGATTT GATTGGCTTA
      ATAACGGGTT GCACTATACC CACCGGTTCT TCTTCCTAAA CTAACCGAAT
4301  TTATGACACC TGGAGTTGGA TTAGATGATA AAGGTGATGG ATTAGGACAA
      AATACTGTGG ACCTCAACCT AATCTACTAT TTCCACTACC TAATCCTGTT
4351  CAATATAGAA CTGTTGATGA AGTTGTTAGC ACTGGAACTG ATATTATCAT
      GTTATATCTT GACAACTACT TCAACAATCG TGACCTTGAC TATAATAGTA
4401  TGTTGGTAGA GGATTGTTTG GTAAAGGAAG AGATCCAGAT ATTGAAGGTA
      ACAACCATCT CCTAACAAAC CATTTCCTTC TCTAGGTCTA TAACTTCCAT
4451  AAAGGTATAG AAATGCTGGT TGGAATGCTT ATTTGAAAAA GACTGGCCAA
      TTTCCATATC TTTACGACCA ACCTTACGAA TAAACTTTTT CTGACCGGTT
4501  TTATAAATGT GAAGGGGGAG ATTTTCACTT TATTAGATTT GTATATATGT
      AATATTTACA CTTCCCCCTC TAAAAGTGAA ATAATCTAAA CATATATACA
4551  AGAATAAATA AATAAATAAG TTAAATAAAT AATTAAATAA GGGTGGTAAT
      TCTTATTTAT TTATTTATTC AATTTATTTA TTAATTTATT CCCACCATTA
4601  TATTACTATT TACAATCAAA GGTGGTCCTT CTAGCTGTAA TCCGGGCAGC
      ATAATGATAA ATGTTAGTTT CCACCAGGAA GATCGACATT AGGCCCGTCG
4651  GCAACGGAAC ATTCATCAGT GTAAAAATGG AATCAATAAA GCCCTGCGCA
      CGTTGCCTTG TAAGTAGTCA CATTTTTACC TTAGTTATTT CGGGACGCGT
4701  GCGCGCAGGG TCAGCCTGAA TACGCGTTTA ATGACCAGCA CAGTCGTGAT
      CGCGCGTCCC AGTCGGACTT ATGCGCAAAT TACTGGTCGT GTCAGCACTA
```

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FIG. 7. (CONTINUED)

```
4751  GGCAAGGTCA GAATAGCCCA AGTCGGCCGA GGGGCCTGTA CAGTGAGGGA
      CCGTTCCAGT CTTATCGGGT TCAGCCGGCT CCCCGGACAT GTCACTCCCT
.....
4801  AGATCTGATA TTGACGAAGA GGAACCAATG TAACGTTACA CTGAAGAAAA
      TCTAGACTAT AACTGCTTCT CCTTGGTTAC ATTGCAATGT GACTTCTTTT
.....
4851  CACACAATAA ACGGGAAGAA ACGGTGTAAA AGTGTGAAAA TAATTTTTGA
      GTGTGTTATT TGCCCTTCTT TGCCACATTT TCACACTTTT ATTAAAAACT
.....
4901  ATATCATTTC CCTTGGTTTA ATTCCAAACG AAACGTGTTT TTTTTAGAGA
      TATAGTAAAG GGAACCAAAT TAAGGTTTGC TTTGCACAAA AAAAATCTCT
.....
          EcoRI                                          ApaLI
          ------                                         -----
4951  ATGGGAATTC TTATTGGATG TCTAGATTGT TTGTTTACTC CAGACTGTGC
      TACCCTTAAG AATAACCTAC AGATCTAACA AACAAATGAG GTCTGACACG
.....
      ApaLI
      --
5001  ACAAAAACGT TTGGATGGAT GATCAGAAGA TATTTTTAGG CTTAGCTCTA
      TGTTTTTGCA AACCTACCTA CTAGTCTTCT ATAAAAATCC GAATCGAGAT
.....
5051  AATATAAGAA ATGATGCTTG AAAAACCAGA CAGAAATTGA GTTTCAAAAA
      TTATATTCTT TACTACGAAC TTTTTGGTCT GTCTTTAACT CAAAGTTTTT
.....
5101  TTGGTAATGT GAGGTATTAG TCAACTAACC AAATAACAAT GCAAACCGGT
      AACCATTACA CTCCATAATC AGTTGATTGG TTTATTGTTA CGTTTGGCCA
.....
5151  TGATACATTT CATTTTGAAA ATAATGAAAC TGGAATTGGA TGACCAGCAC
      ACTATGTAAA GTAAAACTTT TATTACTTTG ACCTTAACCT ACTGGTCGTG
.....
5201  ACAAACACAT AAAGTAATTA TGGGAATTAG AAGCGAACAT AGAGGAGTAC
      TGTTTGTGTA TTTCATTAAT ACCCTTAATC TTCGCTTGTA TCTCCTCATG
.....
5251  TTGGCCACGA ACAGAATACA AGTGGGAACA CTATTTTCTC CATTGTTTTA
      AACCGGTGCT TGTCTTATGT TCACCCTTGT GATAAAAGAG GTAACAAAAT
.....
5301  GTTCTGTTTT TTTGTCAGCC TAGTTTTGTG CTATGTGTAA AAAATATTGC
      CAAGACAAAA AAACAGTCGG ATCAAAACAC GATACACATT TTTTATAACG
.....
            HindIII
            --------
5351  CAAGAAAAAA AGCTTGTTTT GTGGCCAGTG TCCGAAAAAA ATTTTGGGGA
      GTTCTTTTTT TCGAACAAAA CACCGGTCAC AGGCTTTTTT TAAAACCCCT
.....
5401  ATCTTCGGAT TAATTTATGT TTTCATTCCA TCGGGGAAAG TGGGGGGGAA
      TAGAAGCCTA ATTAAATACA AAAGTAAGGT AGCCCCTTTC ACCCCCCCTT
.....
5451  AAAATTTTAA GCAGTTCACA AAACCTTCCA AAAAATATAT GGACAAAGAT
      TTTTAAAATT CGTCAAGTGT TTTGGAAGGT TTTTTATATA CCTGTTTCTA
.....
5501  GATTGTATTT TCCCGACACC AAAATCATAA TTAATTATGA GAAAGTTAAA
      CTAACATAAA AGGGCTGTGG TTTTAGTATT AATTAATACT CTTTCAATTT
.....
5551  TGTAACGTTA CAATTTATGT TTATTTGAAG GTGAAAAGCG ATTTATGATT
      ACATTGCAAT GTTAAATACA AATAAACTTC CACTTTTCGC TAAATACTAA
.....
5601  TTTCCGAAAT GAAAATTTTT TTTAGGTTTA TTTTTTTTGT CGGGCAAAGA
      AAAGGCTTTA CTTTTAAAAA AAATCCAAAT AAAAAAAACA GCCCGTTTCT
.....
```

FIG. 7 (CONTINUED)

```
                                                          Ec RI
                                                          ~
5651  AAAACTGAAC AAGGATTATT AAAATTTTTG GTGTTTGTTT GTGTCTGGAG
      TTTTGACTTG TTCCTAATAA TTTTAAAAAC CACAAACAAA CACAGACCTC
 .....

      EcoRI
      ------
5701  AATTCATTCC TCTCTCATCT TCACACAATG TTTAGACATC TGACACGATT
      TTAAGTAAGG AGAGAGTAGA AGTGTGTTAC AAATCTGTAG ACTGTGCTAA
 .....

5751  CATGATAGTT CGGTTTCCGG GGTTGGTGTT TAGTTTTCGT TTTTCTTTTT
      GTACTATCAA GCCAAAGGCC CCAACCACAA ATCAAAAGCA AAAAGAAAAA
 .....

5801  TTTTGGAAAG AATGTTTTAG CTCATTGGTT TTCTTTCTTC ATTCAATAGT
      AAAACCTTTC TTACAAAATC GAGTAACCAA AAGAAAGAAG TAAGTTATCA
 .....

5851  TTTGAAAGAA TTTGCCCACT TGTTATTACA ATCATATAAA ATTAAACTTT
      AAACTTTCTT AAACGGGTGA ACAATAATGT TAGTATATTT TAATTTGAAA
 .....

5901  GATATAAAAT AGAGTTTGAA AGTTTCCCAG ATCCTTTTTG ATTTCTTTGT
      CTATATTTTA TCTCAAACTT TCAAAGGGTC TAGGAAAAAC TAAAGAAACA
 .....

5951  AAATTTTTTT TTCTCCCACA TATACACACA TACAAACCGA TTTTTATAAG
      TTTAAAAAAA AAGAGGGTGT ATATGTGTGT ATGTTTGGCT AAAAATATTC
 .....

                    PstI          AvaI    BamHI
                    ------        ------------
6001  AAAGAGTTAT ACCCTGCAGC TCGACCTCGA GGGATCCGGG CCCTCTAGAT
      TTTCTCAATA TGGGACGTCG AGCTGGAGCT CCCTAGGCCC GGGAGATCTA
 .....

                    AvaI
                    ------
6051  GCGGCCGCTA GGCCTCGAGG GACTTTTGCA CCAAAAATAA TTTATTTTCC
      CGCCGGCGAT CCGGAGCTCC CTGAAAACGT GGTTTTTATT AAATAAAAGG
 .....

6101  AAAATAAAAT TTAAATAAAT AAAAATAACT CATAATTTAA TAAAAATTTC
      TTTTATTTTA AATTTATTTA TTTTTATTGA GTATTAAATT ATTTTTAAAG
 .....

6151  AAAATCTTCT AGTGTCCTTT CATATGCAGT ACATTAGCCA TCAGTCACTT
      TTTTAGAAGA TCACAGGAAA GTATACGTCA TGTAATCGGT AGTCAGTGAA
 .....

6201  AAACAGCATC TGCTGGTTGA AGAATGCTTG AAGCAATTGT CCAGTCCCAG
      TTTGTCGTAG ACGACCAACT TCTTACGAAC TTCGTTAACA GGTCAGGGTC
 .....

6251  AGGCACAGGC TAGGAGATCT TCAGTTTCGG AGGTAACCTG TAAGTCTGTT
      TCCGTGTCCG ATCCTCTAGA AGTCAAAGCC TCCATTGGAC ATTCAGACAA
 .....

6301  AATGAAGTAA AAGTTCCTTA GGATTTCCAC TCTGACTATG GTCCAGGCAC
      TTACTTCATT TTCAAGGAAT CCTAAAGGTG AGACTGATAC CAGGTCCGTG
 .....

6351  AGTGACTGTA CTCCTTGGCC TTCAGGTAAT GCAGAATCCT CCCATAATAT
      TCACTGACAT GAGGAACCGG AAGTCCATTA CGTCTTAGGA GGGTATTATA
 .....

6401  CTTTTCAGGT GCAGACTGCT CATGAGTTTT CCCCTGGTGA AATCTTCTTT
      GAAAAGTCCA CGTCTGACGA GTACTCAAAA GGGGACCACT TTAGAAGAAA
 .....

6451  CTCCAGTTTT TCTTCCAGGA CTGTCTTCAG ATGGTTTATC TGATGATAGA
      GAGGTCAAAA AGAAGGTCCT GACAGAAGTC TACCAAATAG ACTACTATCT
 .....

6501  CATTAGCCAG GAGGTTCTCA ACAATAGTCT CATTCCAGCC AGTGCTAGAT
      GTAATCGGTC CTCCAAGAGT TGTTATCAGA GTAAGGTCGG TCACGATCTA
 .....
```

FIG. 7. (CONTINUED)

```
6551  GAATCTTGTC TGAAAATAGC AAAGATGTTC TGGAGCATCT CATAGATGGT
      CTTAGAACAG ACTTTTATCG TTTCTACAAG ACCTCGTAGA GTATCTACCA
.....

                                    PstI
                                    --------
6601  CAATGCGGCG TCCTCCTTCT GGAACTGCTG CAGCTGCTTA ATCTCCTCAG
      GTTACGCCGC AGGAGGAAGA CCTTGACGAC GTCGACGAAT TAGAGGAGTC
.....

6651  GGATGTCAAA GTTCATCCTG TCCTTGAGGC AGTATTCAAG CCTCCCATTC
      CCTACAGTTT CAAGTAGGAC AGGAACTCCG TCATAAGTTC GGAGGGTAAG
.....

6701  AATTGCCACA GGAGCTTCTG ACACTGAAAA TTGCTGCTTC TTTGTAGGAA
      TTAACGGTGT CCTCGAAGAC TGTGACTTTT AACGACGAAG AAACATCCTT
.....

6751  TCCAAGCAAG TTGTAGCTCA TGGAAAGAGC TGTAGTGGAG AAGCACAACA
      AGGTTCGTTC AACATCGAGT ACCTTTCTCG ACATCACCTC TTCGTGTTGT
.....

                                                AvaI
                                                --------
6801  GGAGAGCAAT TTGGAGGAGA CACTTGTTGG TCATGTTCCT CGAGGCCTTT
      CCTCTCGTTA AACCTCCTCT GTGAACAACC AGTACAAGGA GCTCCGGAAA
.....

                                                      BamHI
                                                      ---
6851  TTGGCCAGCT GGCGCCTGCT GCGCGACGGC GAGCTGCTCA CCACCCAGGA
      AACCGGTCGA CCGCGGACGA CGCGCTGCCG CTCGACGAGT GGTGGGTCCT
.....

      BamHI
      ---
6901  TCCGTCCCCC TTTTCCTTTG TCGATATCAT GTAATTAGTT ATGTCACGCT
      AGGCAGGGGG AAAAGGAAAC AGCTATAGTA CATTAATCAA TACAGTGCGA
.....

6951  TACATTCACG CCCTCCCCCC ACATCCGCTC TAACCGAAAA GGAAGGAGTT
      ATGTAAGTGC GGGAGGGGGG TGTAGGCGAG ATTGGCTTTT CCTTCCTCAA
.....

7001  AGACAACCTG AAGTCTAGGT CCCTATTTAT TTTTTTATAG TTATGTTAGT
      TCTGTTGGAC TTCAGATCCA GGGATAAATA AAAAAATATC AATACAATCA
.....

7051  ATTAAGAACG TTATTTATAT TTCAAATTTT TCTTTTTTTT CTGTACAGAC
      TAATTCTTGC AATAAATATA AAGTTTAAAA AGAAAAAAAA GACATGTCTG
.....

7101  GCGTGTACGC ATGTAACATT ATACTGAAAA CCTTGCTTGA GAAGGTTTTG
      CGCACATGCG TACATTGTAA TATGACTTTT GGAACGAACT CTTCCAAAAC
.....

                          HindIII
                          -------
7151  GGACGCTCGA AGGCTTTAAT TTGCA
      CCTGCGAGCT TCCGAAATTA AACGT
.....
```

FIG. 8.

```
   1  TTCCATCGGG GAAAGTGGGG GGGAAAAAAT TTTAAGCAGT TCACAAAACC
      AAGGTAGCCC CTTTCACCCC CCCTTTTTTA AAATTCGTCA AGTGTTTTGG
 ..........................................................................
  51  TTCCAAAAAA TATATGGACA AAGATGATTG TATTTTCCCG ACACCAAAAT
      AAGGTTTTTT ATATACCTGT TTCTACTAAC ATAAAAGGGC TGTGGTTTTA
 ..........................................................................
 101  CATAATTAAT TATGAGAAAG TTAAATGTAA CGTTACAATT TATGTTTATT
      GTATTAATTA ATACTCTTTC AATTTACATT GCAATGTTAA ATACAAATAA
 ..........................................................................
 151  TGAAGGTGAA AAGCGATTTA TGATTTTTCC GAAATGAAAA TTTTTTTTAG
      ACTTCCACTT TTCGCTAAAT ACTAAAAAGG CTTTACTTTT AAAAAAAATC
 ..........................................................................
 201  GTTTATTTTT TTTGTCGGGC AAAGAAAAAC TGAACAAGGA TTATTAAAAT
      CAAATAAAAA AAACAGCCCG TTTCTTTTTG ACTTGTTCCT AATAATTTTA
 ..........................................................................
                                EcoRI
                                ------
 251  TTTTGGTGTT TGTTTGTGTC TGGAGAATTC ATTCCTCTCT CATCTTCACA
      AAAACCACAA ACAAACACAG ACCTCTTAAG TAAGGAGAGA GTAGAAGTGT
 ..........................................................................
 301  CAATGTTTAG ACATCTGACA CGATTCATGA TAGTTCGGTT TCCGGGGTTG
      GTTACAAATC TGTAGACTGT GCTAAGTACT ATCAAGCCAA AGGCCCCAAC
 ..........................................................................
 351  GTGTTTAGTT TTCGTTTTTC TTTTTTTTTG GAAAGAATGT TTTAGCTCAT
      CACAAATCAA AAGCAAAAAG AAAAAAAAAC CTTTCTTACA AAATCGAGTA
 ..........................................................................
 401  TGGTTTTCTT TCTTCATTCA ATAGTTTTGA AAGAATTTGC CCACTTGTTA
      ACCAAAAGAA AGAAGTAAGT TATCAAAACT TTCTTAAACG GGTGAACAAT
 ..........................................................................
 451  TTACAATCAT ATAAAATTAA ACTTTGATAT AAAATAGAGT TTGAAAGTTT
      AATGTTAGTA TATTTTAATT TGAAACTATA TTTTATCTCA AACTTTCAAA
 ..........................................................................
 501  CCCAGATCCT TTTTGATTTC TTTGTAAATT TTTTTTTCTC CCACATATAC
      GGGTCTAGGA AAAACTAAAG AAACATTTAA AAAAAAAGAG GGTGTATATG
 ..........................................................................
                                                PstI
                                                --------
 551  ACACATACAA ACCGATTTTT ATAAGAAAGA GTTATACCCT GCAGCTCGAC
      TGTGTATGTT TGGCTAAAAA TATTCTTTCT CAATATGGGA CGTCGAGCTG
 ..........................................................................
                  PstI          HindIII                AvaI
                  -------       --------               -----
 601  CTCGACTGTT TAAACCTGCA GGCATGCAAG CTTGGCCAAA AAGGCCTCGA
      GAGCTGACAA ATTTGGACGT CCGTACGTTC GAACCGGTTT TTCCGGAGCT
 ..........................................................................
      AvaI
      -
 651  GGAACATGAC CAACAAGTGT CTCCTCCAAA TTGCTCTCCT GTTGTGCTTC
      CCTTGTACTG GTTGTTCACA GAGGAGGTTT AACGAGAGGA CAACACGAAG
 ..........................................................................
 701  TCCACTACAG CTCTTTCCAT GAGCTACAAC TTGCTTGGAT TCCTACAAAG
      AGGTGATGTC GAGAAAGGTA CTCGATGTTG AACGAACCTA AGGATGTTTC
 ..........................................................................
 751  AAGCAGCAAT TTTCAGTGTC AGAAGCTCCT GTGGCAATTG AATGGGAGGC
      TTCGTCGTTA AAAGTCACAG TCTTCGAGGA CACCGTTAAC TTACCCTCCG
 ..........................................................................
 801  TTGAATACTG CCTCAAGGAC AGGATGAACT TTGACATCCC TGAGGAGATT
      AACTTATGAC GGAGTTCCTG TCCTACTTGA AACTGTAGGG ACTCCTCTAA
 ..........................................................................
```

FIG. 8. (CONTINUED)

```
                PstI
                -------
 851  AAGCAGCTGC AGCAGTTCCA GAAGGAGGAC GCCGCATTGA CCATCTATGA
      TTCGTCGACG TCGTCAAGGT CTTCCTCCTG CGGCGTAACT GGTAGATACT
 ....................................................................
 901  GATGCTCCAG AACATCTTTG CTATTTTCAG ACAAGATTCA TCTAGCACTG
      CTACGAGGTC TTGTAGAAAC GATAAAAGTC TGTTCTAAGT AGATCGTGAC
 ....................................................................
 951  GCTGGAATGA GACTATTGTT GAGAACCTCC TGGCTAATGT CTATCATCAG
      CGACCTTACT CTGATAACAA CTCTTGGAGG ACCGATTACA GATAGTAGTC
 ....................................................................
1001  ATAAACCATC TGAAGACAGT CCTGGAAGAA AAACTGGAGA AAGAAGATTT
      TATTTGGTAG ACTTCTGTCA GGACCTTCTT TTTGACCTCT TTCTTCTAAA
 ....................................................................
1051  CACCAGGGGA AAACTCATGA GCAGTCTGCA CCTGAAAAGA TATTATGGGA
      GTGGTCCCCT TTTGAGTACT CGTCAGACGT GGACTTTTCT ATAATACCCT
 ....................................................................
1101  GGATTCTGCA TTACCTGAAG GCCAAGGAGT ACAGTCACTG TGCCTGGACC
      CCTAAGACGT AATGGACTTC CGGTTCCTCA TGTCAGTGAC ACGGACCTGG
 ....................................................................
1151  ATAGTCAGAG TGGAAATCCT AAGGAACTTT TACTTCATTA ACAGACTTAC
      TATCAGTCTC ACCTTTAGGA TTCCTTGAAA ATGAAGTAAT TGTCTGAATG
 ....................................................................
1201  AGGTTACCTC CGAAACTGAA GATCTCCTAG CCTGTGCCTC TGGGACTGGA
      TCCAATGGAG GCTTTGACTT CTAGAGGATC GGACACGGAG ACCCTGACCT
 ....................................................................
1251  CAATTGCTTC AAGCATTCTT CAACCAGCAG ATGCTGTTTA AGTGACTGAT
      GTTAACGAAG TTCGTAAGAA GTTGGTCGTC TACGACAAAT TCACTGACTA
 ....................................................................
1301  GGCTAATGTA CTGCATATGA AAGGACACTA GAAGATTTTG AAATTTTTAT
      CCGATTACAT GACGTATACT TTCCTGTGAT CTTCTAAAAC TTTAAAAATA
 ....................................................................
1351  TAAATTATGA GTTATTTTTA TTTATTTAAA TTTTATTTTG GAAAATAAAT
      ATTTAATACT CAATAAAAAT AAATAAATTT AAAATAAAAC CTTTTATTTA
 ....................................................................

                                                        XmaI
                                                        -
                                                        SmaI
                                                        -
                                                        BamHI
                                                        -------
                                  AvaI                  AvaI
                                  ------                -
1401  TATTTTTGGT GCAAAAGTCC CTCGAGGCCT AGCGGCCGCC TAGAGGATCC
      ATAAAAACCA CGTTTTCAGG GAGCTCCGGA TCGCCGGCGG ATCTCCTAGG
 ....................................................................
      XmaI
      ------
      SmaI
      ------
      AvaI
      ------
1451  CCGGGCGCTA GGCGGCCGCT AGGCCTTTTT GGCCAAGCTC GAATTTCGAG
      GGCCCGCGAT CCGCCGGCGA TCCGGAAAAA CCGGTTCGAG CTTAAAGCTC
 ....................................................................
                        XmaI
                        -------
                        SmaI
                        -------
      EcoRI             AvaI      ClaI
      ------            -------   ------
1501  GAATTCGAGC TCGGTACCCG GGGGATCGAT CCGTCCCCCT TTTCCTTTGT
      CTTAAGCTCG AGCCATGGGC CCCCTAGCTA GGCAGGGGGA AAAGGAAACA
 ....................................................................
```

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FIG. 8 (CONTINUED)

```
1551  CGATATCATG TAATTAGTTA TGTCACGCTT ACATTCACGC CCTCCCCCCA
      GCTATAGTAC ATTAATCAAT ACAGTGCGAA TGTAAGTGCG GGAGGGGGT
.....

1601  CATCCGCTCT AACCGAAAAG GAAGGAGTTA GACAACCTGA AGTCTAGGTC
      GTAGGCGAGA TTGGCTTTTC CTTCCTCAAT CTGTTGGACT TCAGATCCAG
.....

1651  CCTATTTATT TTTTTATAGT TATGTTAGTA TTAAGAACGT TATTTATATT
      GGATAAATAA AAAAATATCA ATACAATCAT AATTCTTGCA ATAAATATAA
.....

1701  TCAAATTTTT CTTTTTTTTC TGTACAGACG CGTGTACGCA TGTAACATTA
      AGTTTAAAAA GAAAAAAAAG ACATGTCTGC GCACATGCGT ACATTGTAAT
.....

1751  TACTGAAAAC CTTGCTTGAG AAGGTTTTGG GACGCTCGAA GGCTTTAATT
      ATGACTTTTG GAACGAACTC TTCCAAAACC CTGCGAGCTT CCGAAATTAA
.....

1801  TGCAAGCTAG CTTGGCGTAA TCATGGTCAT AGCTGTTTCC TGTGTGAAAT
      ACGTTCGATC GAACCGCATT AGTACCAGTA TCGACAAAGG ACACACTTTA
.....

1851  TGTTATCCGC TCACAATTCC ACACAACATA CGAGCCGGAA GCATAAAGTG
      ACAATAGGCG AGTGTTAAGG TGTGTTGTAT GCTCGGCCTT CGTATTTCAC
.....

1901  TAAAGCCTGG GGTGCCTAAT GAGTGAGCTA ACTCACATTA ATTGCGTTGC
      ATTTCGGACC CCACGGATTA CTCACTCGAT TGAGTGTAAT TAACGCAACG
.....

1951  GCTCACTGCC CGCTTTCCAG TCGGGAAACC TGTCGTGCCA GAGATCTCTG
      CGAGTGACGG GCGAAAGGTC AGCCCTTTGG ACAGCACGGT CTCTAGAGAC
.....

2001  CATTAATGAA TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGGCG
      GTAATTACTT AGCCGGTTGC GCGCCCCTCT CCGCCAAACG CATAACCCGC
.....

2051  CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC GTTCGGCTGC
      GAGAAGGCGA AGGAGCGAGT GACTGAGCGA CGCGAGCCAG CAAGCCGACG
.....

                    ClaI
                    -------
2101  GGCGAGCGGT ATCAGATCGA TCTCACTCAA AGGCGGTAAT ACGGTTATCC
      CCGCTCGCCA TAGTCTAGCT AGAGTGAGTT TCCGCCATTA TGCCAATAGG
.....

2151  ACAGAATCAG GGGATAACGC AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA
      TGTCTTAGTC CCCTATTGCG TCCTTTCTTG TACACTCGTT TTCCGGTCGT
.....

2201  AAAGGCCAGG AACCGTAAAA AGGCCGCGTT GCTGGCGTTT TTCCATAGGC
      TTTCCGGTCC TTGGCATTTT TCCGGCGCAA CGACCGCAAA AAGGTATCCG
.....

2251  TCCGCCCCCC TGACGAGCAT CACAAAAATC GACGCTCAAG TCAGAGGTGG
      AGGCGGGGGG ACTGCTCGTA GTGTTTTTAG CTGCGAGTTC AGTCTCCACC
.....

2301  CGAAACCCGA CAGGACTATA AAGATACCAG GCGTTTCCCC CTGGAAGCTC
      GCTTTGGGCT GTCCTGATAT TTCTATGGTC CGCAAAGGGG GACCTTCGAG
.....

2351  CCTCGTGCGC TCTCCTGTTC CGACCCTGCC GCTTACCGGA TACCTGTCCG
      GGAGCACGCG AGAGGACAAG GCTGGGACGG CGAATGGCCT ATGGACAGGC
.....

2401  CCTTTCTCCC TTCGGGAAGC GTGGCGCTTT CTCATAGCTC ACGCTGTAGG
      GGAAAGAGGG AAGCCCTTCG CACCGCGAAA GAGTATCGAG TGCGACATCC
.....

                                                    ApaLI
                                                    ------
2451  TATCTCAGTT CGGTGTAGGT CGTTCGCTCC AAGCTGGGCT GTGTGCACGA
      ATAGAGTCAA GCCACATCCA GCAAGCGAGG TTCGACCCGA CACACGTGCT
.....
```

FIG. 8. (CONTINUED)

```
2501  ACCCCCCGTT CAGCCCGACC GCTGCGCCTT ATCCGGTAAC TATCGTCTTG
      TGGGGGGCAA GTCGGGCTGG CGACGCGGAA TAGGCCATTG ATAGCAGAAC
.....
2551  AGTCCAACCC GGTAAGACAC GACTTATCGC CACTGGCAGC AGCCACTGGT
      TCAGGTTGGG CCATTCTGTG CTGAATAGCG GTGACCGTCG TCGGTGACCA
.....
2601  AACAGGATTA GCAGAGCGAG GTATGTAGGC GGTGCTACAG AGTTCTTGAA
      TTGTCCTAAT CGTCTCGCTC CATACATCCG CCACGATGTC TCAAGAACTT
.....
2651  GTGGTGGCCT AACTACGGCT ACACTAGAAG GACAGTATTT GGTATCTGCG
      CACCACCGGA TTGATGCCGA TGTGATCTTC CTGTCATAAA CCATAGACGC
.....
2701  CTCTGCTGAA GCCAGTTACC TTCGGAAAAA GAGTTGGTAG CTCTTGATCC
      GAGACGACTT CGGTCAATGG AAGCCTTTTT CTCAACCATC GAGAACTAGG
.....
2751  GGCAAACAAA CCACCGCTGG TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA
      CCGTTTGTTT GGTGGCGACC ATCGCCACCA AAAAAACAAA CGTTCGTCGT
.....
2801  GATTACGCGC AGAAAAAAAG GATCTCAAGA AGATCCTTTG ATCTTTTCTA
      CTAATGCGCG TCTTTTTTTC CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT
.....
2851  CGGGGTCTGA CGCTCAGTGG AACGAAAACT CACGTTAAGG GATTTTGGTC
      GCCCCAGACT GCGAGTCACC TTGCTTTTGA GTGCAATTCC CTAAAACCAG
.....
2901  ATGAGATTAT CAAAAAGGAT CTTCACCTAG ATCCTTTTAA ATTAAAAATG
      TACTCTAATA GTTTTTCCTA GAAGTGGATC TAGGAAAATT TAATTTTTAC
.....
2951  AAGTTTTAAA TCAATCTAAA GTATATATGA GTAAACTTGG TCTGACAGTT
      TTCAAAATTT AGTTAGATTT CATATATACT CATTTGAACC AGACTGTCAA
.....
3001  ACCAATGCTT AATCAGTGAG GCACCTATCT CAGCGATCTG TCTATTTCGT
      TGGTTACGAA TTAGTCACTC CGTGGATAGA GTCGCTAGAC AGATAAAGCA
.....
3051  TCATCCATAG TTGCCTGACT CCCCGTCGTG TAGATAACTA CGATACGGGA
      AGTAGGTATC AACGGACTGA GGGGCAGCAC ATCTATTGAT GCTATGCCCT
.....
3101  GGGCTTACCA TCTGGCCCCA GTGCTGCAAT GATACCGCGA GACCCACGCT
      CCCGAATGGT AGACCGGGGT CACGACGTTA CTATGGCGCT CTGGGTGCGA
.....
3151  CACCGGCTCC AGATTTATCA GCAATAAACC AGCCAGCCGG AAGGGCCGAG
      GTGGCCGAGG TCTAAATAGT CGTTATTTGG TCGGTCGGCC TTCCCGGCTC
.....
3201  CGCAGAAGTG GTCCTGCAAC TTTATCCGCC TCCATCCAGT CTATTAATTG
      GCGTCTTCAC CAGGACGTTG AAATAGGCGG AGGTAGGTCA GATAATTAAC
.....
3251  TTGCCGGGAA GCTAGAGTAA GTAGTTCGCC AGTTAATAGT TTGCGCAACG
      AACGGCCCTT CGATCTCATT CATCAAGCGG TCAATTATCA AACGCGTTGC
.....
3301  TTGTTGCCAT TGCTACAGGC ATCGTGGTGT CACGCTCGTC GTTTGGTATG
      AACAACGGTA ACGATGTCCG TAGCACCACA GTGCGAGCAG CAAACCATAC
.....
3351  GCTTCATTCA GCTCCGGTTC CCAACGATCA AGGCGAGTTA CATGATCCCC
      CGAAGTAAGT CGAGGCCAAG GGTTGCTAGT TCCGCTCAAT GTACTAGGGG
.....
3401  CATGTTGTGC AAAAAAGCGG TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA
      GTACAACACG TTTTTTCGCC AATCGAGGAA GCCAGGAGGC TAGCAACAGT
.....
3451  GAAGTAAGTT GGCCGCAGTG TTATCACTCA TGGTTATGGC AGCACTGCAT
      CTTCATTCAA CCGGCGTCAC AATAGTGAGT ACCAATACCG TCGTGACGTA
.....
```

FIG. 8. (CONTINUED)

```
3501  AATTCTCTTA CTGTCATGCC ATCCGTAAGA TGCTTTTCTG TGACTGGTGA
      TTAAGAGAAT GACAGTACGG TAGGCATTCT ACGAAAAGAC ACTGACCACT
.....
3551  GTACTCAACC AAGTCATTCT GAGAATAGTG TATGCGGCGA CCGAGTTGCT
      CATGAGTTGG TTCAGTAAGA CTCTTATCAC ATACGCCGCT GGCTCAACGA
.....
3601  CTTGCCCGGC GTCAATACGG GATAATACCG CGCCACATAG CAGAACTTTA
      GAACGGGCCG CAGTTATGCC CTATTATGGC GCGGTGTATC GTCTTGAAAT
.....
3651  AAAGTGCTCA TCATTGGAAA ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT
      TTTCACGAGT AGTAACCTTT TGCAAGAAGC CCCGCTTTTG AGAGTTCCTA
.....
                                                  ApaLI
                                                  -------
3701  CTTACCGCTG TTGAGATCCA GTTCGATGTA ACCCACTCGT GCACCCAACT
      GAATGGCGAC AACTCTAGGT CAAGCTACAT TGGGTGAGCA CGTGGGTTGA
.....
3751  GATCTTCAGC ATCTTTTACT TTCACCAGCG TTTCTGGGTG AGCAAAAACA
      CTAGAAGTCG TAGAAAATGA AAGTGGTCGC AAAGACCCAC TCGTTTTTGT
.....
3801  GGAAGGCAAA ATGCCGCAAA AAAGGGAATA AGGGCGACAC GGAAATGTTG
      CCTTCCGTTT TACGGCGTTT TTTCCCTTAT TCCCGCTGTG CCTTTACAAC
.....
3851  AATACTCATA CTCTTCCTTT TTCAATATTA TTGAAGCATT TATCAGGGTT
      TTATGAGTAT GAGAAGGAAA AAGTTATAAT AACTTCGTAA ATAGTCCCAA
.....
3901  ATTGTCTCAT GAGCGGATAC ATATTTGAAT GTATTTAGAA AAATAAACAA
      TAACAGAGTA CTCGCCTATG TATAAACTTA CATAAATCTT TTTATTTGTT
.....
3951  ATAGGGGTTC CGCGCACATT TCCCCGAAAA GTGCCACCTG ACGTCTAAGA
      TATCCCCAAG GCGCGTGTAA AGGGGCTTTT CACGGTGGAC TGCAGATTCT
.....
4001  AACCATTATT ATCATGACAT TAACCTATAA AAATAGGCGT ATCACGAGGC
      TTGGTAATAA TAGTACTGTA ATTGGATATT TTTATCCGCA TAGTGCTCCG
.....
4051  CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG
      GGAAAGCAGA GCGCGCAAAG CCACTACTGC CACTTTTGGA GACTGTGTAC
.....
4101  CAGCTCCCGG AGACGGTCAC AGCTTGTCTG TAAGCGGATG CCGGGAGCAG
      GTCGAGGGCC TCTGCCAGTG TCGAACAGAC ATTCGCCTAC GGCCCTCGTC
.....
4151  ACAAGCCCGT CAGGGCGCGT CAGCGGGTGT TGGCGGGTGT CGGGGCTGGC
      TGTTCGGGCA GTCCCGCGCA GTCGCCCACA ACCGCCCACA GCCCCGACCG
.....
                                            ApaLI
                                            -------
4201  TTAACTATGC GGCATCAGAG CAGATTGTAC TGAGAGTGCA CCATATCGAC
      AATTGATACG CCGTAGTCTC GTCTAACATG ACTCTCACGT GGTATAGCTG
.....
4251  GCTCTCCCTT ATGCGACTCC TGCATTAGGA AGCAGCCCAG TAGTAGGTTG
      CGAGAGGGAA TACGCTGAGG ACGTAATCCT TCGTCGGGTC ATCATCCAAC
.....
4301  AGGCCGTTGA GCACCGCCGC CGCAAGGAAT GGTGCATGCA AGGAGATGGC
      TCCGGCAACT CGTGGCGGCG GCGTTCCTTA CCACGTACGT TCCTCTACCG
.....
4351  GCCCAACAGT CCCCCGGCCA CGGGGCCTGC CACCATACCC ACGCCGAAAC
      CGGGTTGTCA GGGGGCCGGT GCCCCGGACG GTGGTATGGG TGCGGCTTTG
.....
4401  AAGCACTAAT AGGAATTGAT TTGGATGGTA TAAACGGAAA CAAAAAAAAG
      TTCGTGATTA TCCTTAACTA AACCTACCAT ATTTGCCTTT GTTTTTTTTC
.....
```

FIG. 8. (CONTINUED)

```
4451  AGCTGGTACT ACTTTCTTTA AAATTATTTT ATTATTTGAT TTTATTTAAT
      TCGACCATGA TGAAAGAAAT TTTAATAAAA TAATAAACTA AAATAAATTA

4501  AGTATATATT ATATTTTGAA CGTAGATTAT TTTGTTGAAA GTTGCTGTAG
      TCATATATAA TATAAAACTT GCATCTAATA AAACAACTTT CAACGACATC

4551  TGCCATTGAT TCGTAACACT AATTCTGTAT TAGTCATTCC TCTTGTTTGA
      ACGGTAACTA AGCATTGTGA TTAAGACATA ATCAGTAAGG AGAACAAACT

4601  TAGTATCCAA AAAAACGGCT ATTTTTTTGC AATCTTATTT CCTGCATATT
      ATCATAGGTT TTTTTGCCGA TAAAAAAACG TTAGAATAAA GGACGTATAA

4651  ATACAGATAA CATAATGAAA GAAAAAATCT TTTTTTTTGT TCTTCAATGA
      TATGTCTATT GTATTACTTT CTTTTTTAGA AAAAAAAACA AGAAGTTACT

4701  TGATTTCAAC CATTCTTTTA AACATTGATC AATTCCTGAG CAACAACCCC
      ACTAAAGTTG GTAAGAAAAT TTGTAACTAG TTAAGGACTC GTTGTTGGGG

4751  ATACACACTG GTTTATATAC CGCCCCTTTT ACAGTTGAAG AAAGAAATAG
      TATGTGTGAC CAAATATATG GCGGGGAAAA TGTCAACTTC TTTCTTTATC

4801  AAATAGAAAT AGCAAACAAA AGATATGACA GTCAACACTA AGACCTATAG
      TTTATCTTTA TCGTTTGTTT TCTATACTGT CAGTTGTGAT TCTGGATATC

4851  TGAGAGAGCA GAAACTCATG CCTCACCAGT AGCACAGCGA TTATTTCGAT
      ACTCTCTCGT CTTTGAGTAC GGAGTGGTCA TCGTGTCGCT AATAAAGCTA

4901  TAATGGAACT GAAGAAAACC AATTTATGTG CATCAATTGA CGTTGATACC
      ATTACCTTGA CTTCTTTTGG TTAAATACAC GTAGTTAACT GCAACTATGG

                  AvaI
                  ------
4951  ACTAAGGAGT TCCTCGAGTT AATTGATAAA TTAGGTCCTT ATGTATGCTT
      TGATTCCTCA AGGAGCTCAA TTAACTATTT AATCCAGGAA TACATACGAA

5001  AATCAAGACT CATATTGATA TAATCAATGA TTTTTCCTAT GAATCCACTA
      TTAGTTCTGA GTATAACTAT ATTAGTTACT AAAAAGGATA CTTAGGTGAT

5051  TTGAACCATT ATTAGAACTT TCACGTAAAC ATCAATTTAT GATTTTTGAA
      AACTTGGTAA TAATCTTGAA AGTGCATTTG TAGTTAAATA CTAAAAACTT

5101  GATAGAAAAT TTGCTGATAT TGGTAATACC GTAAAGAAAC AATATATTGG
      CTATCTTTTA AACGACTATA ACCATTATGG CATTTCTTTG TTATATAACC

5151  TGGAGTTTAT AAAATTAGTA GTTGGGCAGA TATTACCAAT GCTCATGGTG
      ACCTCAAATA TTTTAATCAT CAACCCGTCT ATAATGGTTA CGAGTACCAC

5201  TCACTGGGAA TGGAGTGGTT GAAGGATTAA AACAGGGAGC TAAAGAAACC
      AGTGACCCTT ACCTCACCAA CTTCCTAATT TTGTCCCTCG ATTTCTTTGG

5251  ACCACCAACC AAGAGCCAAG AGGGTTATTG ATGTTAGCTG AATTATCATC
      TGGTGGTTGG TTCTCGGTTC TCCCAATAAC TACAATCGAC TTAATAGTAG

5301  AGTGGGATCA TTAGCATATG GAGAATATTC TCAAAAAACT GTTGAAATTG
      TCACCCTAGT AATCGTATAC CTCTTATAAG AGTTTTTTGA CAACTTTAAC

5351  CTAAATCCGA TAAGGAATTT GTTATTGGAT TTATTGCCCA ACGTGATATG
      GATTTAGGCT ATTCCTTAAA CAATAACCTA AATAACGGGT TGCACTATAC
```

FIG. 8. (CONTINUED) 25/63

```
5401  GGTGGCCAAG AAGAAGGATT TGATTGGCTT ATTATGACAC CTGGAGTTGG
      CCACCGGTTC TTCTTCCTAA ACTAACCGAA TAATACTGTG GACCTCAACC
5451  ATTAGATGAT AAAGGTGATG GATTAGGACA ACAATATAGA ACTGTTGATG
      TAATCTACTA TTTCCACTAC CTAATCCTGT TGTTATATCT TGACAACTAC
5501  AAGTTGTTAG CACTGGAACT GATATTATCA TTGTTGGTAG AGGATTGTTT
      TTCAACAATC GTGACCTTGA CTATAATAGT AACAACCATC TCCTAACAAA
5551  GGTAAAGGAA GAGATCCAGA TATTGAAGGT AAAAGGTATA GAAATGCTGG
      CCATTTCCTT CTCTAGGTCT ATAACTTCCA TTTTCCATAT CTTTACGACC
5601  TTGGAATGCT TATTTGAAAA AGACTGGCCA ATTATAAATG TGAAGGGGGA
      AACCTTACGA ATAAACTTTT TCTGACCGGT TAATATTTAC ACTTCCCCCT
5651  GATTTTCACT TTATTAGATT TGTATATATG TAGAATAAAT AAATAAATAA
      CTAAAAGTGA AATAATCTAA ACATATATAC ATCTTATTTA TTTATTTATT
5701  GTTAAATAAA TAATTAAATA AGGGTGGTAA TTATTACTAT TTACAATCAA
      CAATTTATTT ATTAATTTAT TCCCACCATT AATAATGATA AATGTTAGTT
5751  AGGTGGTCCT TCTAGCTGTA ATCCGGGCAG CGCAACGGAA CATTCATCAG
      TCCACCAGGA AGATCGACAT TAGGCCCGTC GCGTTGCCTT GTAAGTAGTC
5801  TGTAAAAATG GAATCAATAA AGCCCTGCGC TCATGAGCCC GAAGTGGCGA
      ACATTTTTAC CTTAGTTATT TCGGGACGCG AGTACTCGGG CTTCACCGCT
5851  GCCCGATCTT CCCCATCGGT GATGTCGGCG ATATAGGCGC CAGCAACCGC
      CGGGCTAGAA GGGGTAGCCA CTACAGCCGC TATATCCGCG GTCGTTGGCG
5901  ACCTGTGGCG CCGCAGCGCG CAGGGTCAGC CTGAATACGC GTTTAATGAC
      TGGACACCGC GGCGTCGCGC GTCCCAGTCG GACTTATGCG CAAATTACTG
5951  CAGCACAGTC GTGATGGCAA GGTCAGAATA GCCCAAGTCG GCCGAGGGGC
      GTCGTGTCAG CACTACCGTT CCAGTCTTAT CGGGTTCAGC CGGCTCCCCG
6001  CTGTACAGTG AGGGAAGATC TGATATTGAC GAAGAGGAAC CAATGTAACG
      GACATGTCAC TCCCTTCTAG ACTATAACTG CTTCTCCTTG GTTACATTGC
6051  TTACACTGAA GAAAACACAC AATAAACGGG AAGAAACGGT GTAAAAGTGT
      AATGTGACTT CTTTTGTGTG TTATTTGCCC TTCTTTGCCA CATTTTCACA
6101  GAAAATAATT TTTGAATATC ATTTCCCTTG GTTTAATTCC AAACGAAACG
      CTTTTATTAA AAACTTATAG TAAAGGGAAC CAAATTAAGG TTTGCTTTGC
                          EcoRI
                          -------
6151  TGTTTTTTTT AGAGAATGGG AATTCTTATT GGATGTCTAG ATTGTTTGTT
      ACAAAAAAAA TCTCTTACCC TTAAGAATAA CCTACAGATC TAACAAACAA
                    ApaLI
                    ------
6201  TACTCCAGAC TGTGCACAAA AACGTTTGGA TGGATGATCA GAAGATATTT
      ATGAGGTCTG ACACGTGTTT TTGCAAACCT ACCTACTAGT CTTCTATAAA
6251  TTAGGCTTAG CTCTAAATAT AAGAAATGAT GCTTGAAAAA CCAGACAGAA
      AATCCGAATC GAGATTTATA TTCTTTACTA CGAACTTTTT GGTCTGTCTT
6301  ATTGAGTTTC AAAAATTGGT AATGTGAGGT ATTAGTCAAC TAACCAAATA
      TAACTCAAAG TTTTTAACCA TTACACTCCA TAATCAGTTG ATTGGTTTAT
```

FIG. 8. (CONTINUED)

```
6351  ACAATGCAAA CCGGTTGATA CATTTCATTT TGAAAATAAT GAAACTGGAA
      TGTTACGTTT GGCCAACTAT GTAAAGTAAA ACTTTTATTA CTTTGACCTT
.....
6401  TTGGATGACC AGCACACAAA CACATAAAGT AATTATGGGA ATTAGAAGCG
      AACCTACTGG TCGTGTGTTT GTGTATTTCA TTAATACCCT TAATCTTCGC
.....
6451  AACATAGAGG AGTACTTGGC CACGAACAGA ATACAAGTGG GAACACTATT
      TTGTATCTCC TCATGAACCG GTGCTTGTCT TATGTTCACC CTTGTGATAA
.....
6501  TTCTCCATTG TTTTAGTTCT GTTTTTTTGT CAGCCTAGTT TTGTGCTATG
      AAGAGGTAAC AAAATCAAGA CAAAAAAACA GTCGGATCAA AACACGATAC
.....
                              HindIII
                              -------
6551  TGTAAAAAAT ATTGCCAAGA AAAAAAGCTT GTTTTGTGGC CAGTGTCCGA
      ACATTTTTTA TAACGGTTCT TTTTTTCGAA CAAAACACCG GTCACAGGCT
.....
6601  AAAAAATTTT GGGGAATCTT CGGATTAATT TATGTTTTCA
      TTTTTTAAAA CCCCTTAGAA GCCTAATTAA ATACAAAAGT
.....
```

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FIG. 9.

ATGTATGTTTATAAGAGAGATGGCCGTAAAGAGCCAGTACGTTTCGACAAAAT
CACTGCCAGAGTTCAAAGATTATGTTA
CGGTTTGAATCCAAACCACGTTGAACCAGTTGCTATTACCCAAAAAGTTATATC
AGGTGTTTACCAGGGGGTTACTACTA
TTGAGTTGGACAACTTGGCTGCAGAAATTGCTGCTACAATGACAACAATTCAC
CCAGATTACGCTGTCTTAGCCGCTAGA
ATTGCCGTATCAAATTTACATAAGCAAACCACCAAACAGTATTCCAAAGTGTC
TAAGGATTTATATGAATACATTAATCC
TAAGACTGGGTTACACTCTCCTATGATTTCCAAGGAAACCTACGACATCATTAT
GGAACACGAAGATGAATTAAACTCAG
CCATTGTTTACGACAGAGATTTTAACTACAATTATTTTGGGTTCAAGACTTTGG
AAAGATCATATTTGTTACGTATCAAC
GGTAAGGTTGCTGAAAGACCACAACATTTGATCATGAGGGTTGCTGTCGGTAT
TCACGGTAATGATATACCAAGGGTCAT
TGAAACCTATAACTTGATGTCTCAAAGATTCTTCACCCATGGTTCTCCTTGTTTA
TTTAACGCTGGTACACCAAGACCAC
AAATGTCCTCATGTTTCTTGCTTGCTATGAAGGATGATTCTATTGAAGGTATTT
ACGACACTTTGAAATCGTGTGCTTTG
ATCTCAAAAAGTGCTGGAGGAATCGGTTTACACATCCACAACATTCGTTCTACC
GGTGCTTACATTGCTGGTACCAATGG
TACTTCTAATGGTATTATTCCAATGGTAAGAGTATTCAATAACACTGCACGTTA
TGTCGACCAAGGTGGTAACAAGAGAC
CTGGTGCCTTTGCCTTGTACTTAGAACCATGGCACAGTGACATTTTTGATTTCA
TTGATATTAGAAAGAATCACGGTAAA
GAAGAAATCAGAGCCAGAGATTTGTTCCCAGCTTTGTGGATTCCAGATTTGTTC
ATGAAAAGAGTTGAACAAAATGGTGA
CTGGACTTTATTCTCACCAAATGAGGCCCCAGGCTTGGCTGATGTTTATGGTGA
CGAATTCGAAGAATTATACACCAAAT
ACGAAAAAGAAAACCGTGGTAGACAGACCATCAAAGCTCAAAAATTGTGGTA
TGCTATTTTGGGAGCCCAAACTGAAACA
GGTACCCCATTTATGTTATATAAAGATTCATGTAACAACAAATCCAACCAAAA
GAACTTGGGTATTATCAAATCTTCCAA
CTTGTGTTGTGAAATTGTTGAATATTCTGCTCCAGATGAAGTTGCTGTTTGTAA
CTTGGCTTCCATTGCCTTGCCATCAT
TTGTTGAAAATGATGAAAAAAGTACTTGGTACAACTTTGACAAATTACATCAG
GTCACTAAGGTTGTCACCCGTAACTTG
AACAGAGTTATTGACCGTAACCATTACCCAGTCCCAGAAGCTGAAAGATCAAA
CATGAGACACAGACCAATTGCTTTGGG
TGTTCAAGGTTTGGCTGATGCCTTTATGGAATTGAGATTACCATTTGACTCTCA
AGAAGCTAGAGAATTGAACATTCAAA

FIG. 9. (CONTINUED)

TTTTTGAGACTATCTACCATGCTGCTGTTGAAGCTTCAATTGAATTGGCTAAAG
AAGAAGGTGCCTACGAAACCTATCCA
GGTTCTCCAGCCTCTCAAGGTTTATTACAATTTGATTTGTGGAACAGAAAACCA
ACTGAATTATGGGATTGGGATACATT
AAAACAAGATTTGGCCAAACATGGTATGAGAAACTCCTTGTTGGTTGCACCAA
TGCCTACTGCTTCCACATCACAAATTT
TGGGTAACAATGAATGTTTTGAACCATACACTTCTAACATTTACTCTAGAAGAG
TATTAGCTGGAGAATTCCAAATTGTC
AATCCATATTTATTGAAGGACTTGGTTGATTTGGGTGTCTGGAACGACGCTATG
AAAAGTAGTATTATTGCTAACAATGG
TTCTATCCAAGCCTTACCAAACATCCCTGATGAAATCAAGGCATTGTACAAAA
CTGTCTGGGAAATCTCACAAAAACATA
TTATCGACATGGCTGCTGATAGAGCAGCATTTATTGATCAATCTCAATCATTAA
ACATTCACATCAAAGATCCAACAATG
GGTAAATTAACCAGTATGCACTTCTACGGTTGGAAGAAAGGTTTAAAGACTGG
TATGTACTACTTAAGAACACAAGCTGC
CAGTGCTGCTATTCAATTTACCATTGATCAAAAGATTGCTGAGACTGCCGGTCA
TACGGTTGCAAACTTGGACAAATTAA

ACATTAAGAAATATGTTAACAAAGGAAGAGTTGAGAGTGAGAATACCAGTGAT
GCTCCATACAAGTCACCATCAACCGAA
CCAACCTCATTAGAAAGTTCAGTTGCTGATTTGAAAATAAAAGATGAAGGTGA
AAAGCCAGCTGAAGACAAAACCATTGA
AGAACTCGAAAATGACATTTATAGTGCCAAAGTTATCGCATGTGCTATTGATA
ATCCAGAATCTTGTACAATGTGTTCTG
GT

FIG. 10.

FIG. 11.

FIG. 12.

CCCCGTTAACCACTTCTAGGGTATACCATTTCATCTGACTGAATAACTGGTTAG
TCGATTTGTTGTTGAAGAAAAGTGAC
CACCTAGTTTTTTCTGCCAACATTTTTTGCGATGAGCCGTCGACGCGTTGTCTTT
TTCTACCCCACGTTTAACAATCTTG
CCAGTCAATTCCCTAGCCAAATAAACTTTAGACTCACAACTCTAACACTGACTC
GTGCCCCCCTGTTTAAACTCTAAATT
ACTTCACAGAGCCTTTACTACCTTAAATTTARGRTTWTSKAKKGTTTCTGTTTTT
TTGCAAATCACCCTGACTYGTTTTT
TTTTCAGCCAGGTTTTTCGTTAAAATCTGACCAAAAAATTTACRACTCCTATWT
TTAAAACTCYAAAWWACAATTAAAAC
TCAATTCAGACAAGTCCTTCTGCTCATTCTGAGTCTTCTCTATTGTCTTTTGACT
TTTTGTGTGTGACTATTTTCATGAT
CACCCCGTTTCTTGCATTTTTTTCAGTCAACTTTTTCTCAAAATCAAGCCAAAAA
AACACACCTTTAACTACCTATACAA
CGCAAACCTATTCAAAACA

FIG. 13.

ATGACTACTTCCAAGGAAACTTTCCTTTTCACTTCAGAATCCGTTGGTGAAGGT
CACCCAGATAAGATTTGTGACCAAGT
CTCCGATGCCATTTTAGATGCTTGTTTAGCTGTTGATCCATTGTCAAAAGTTGCT
TGTGAAACTGCTGCCAAAACCGGTA
TGATTATGGTTTTTGGTGAAATTACCACTAAAGCTCAATTGGATTATCAAAAAA
TCATTAGAGACACCATTAAACACATT
GGTTACGACGATTCTGAAAAAGGTTTTGATTACAAGACTTGTAACGTCTTGGTT
GCAATTGAACAACAATCTCCAGATAT
TGCTCAAGGTTTACATTACGAAAAAGCTTTGGAAGAGTTGGGTGCTGGTGATC
AAGGTATTATGTTTGGTTATGCCACCG
ATGAAACCGATGAAAAATTGCCATTGACCATTTTATTGGCCCACAAATTGAAT
GCTGCCTTGGCTTCTGCCAGAAGATCA
GGTTCCTTGCCATGGTTGAGACCAGATACCAAAACCCAAGTCACCATCGAGTA
TGAAAAAGATGGTGGTGCAGTTATCCC
AAAAAGAGTCGACACAATTGTTATTTCCACTCAACATGCCGAAGAAATCACCA
CCGAAAATTTGAGAAAAGAAATTATTG
AACATATCATCAAGCAAGTCATCCCAGAACATTTATTAGACGACAAAACTATC
TACCACATTCAGCCATCAGGCAGATTC
GTCATTGGTGGTCCCCAAGGTGATGCTGGTTTGACTGGTAGAAAGATCATTGTT
GACACCTATGGTGGTTGGGGTGCACA
TGGTGGTGGTGCCTTCTCAGGCAAGGATTTCTCCAAAGTTGATAGGTCTGCTGC
TTATGCCGCTCGGTGGGTTGCTAAGT
CGTTGGTGACCGCCGGATTGGCCAAAAGGGCCTTGGTGCAGTTCTCCTATGCTA
TTGGGGTTGCTGAACCCACCAGCATT
TATATAGACACCTATGGGACATCTAAATTGAGCACCGAAGCCCTTGTAGAAAT
TATCAAGAATAATTTTGACTTACGCCC
TGGCGTAATTGTAAAAGAATTAGATTTGGCTCGTCCTATTTATTTTAAAACCGC
TTCTTACGGACATTTTACTAACCAAG
AAAATTCTTGGGAACAACCAAAAAAATTAAAATTT

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FIG. 14.

```
  1 MVVYKRDGRK EPVRFDKITA RVGRLCYGLN PMHVEPVAIT QKVISGVKDG
 51 VTTIELDNLA AELAATMTTI HPDYAVLAAR IAVSNLHKQT TKQYSKVSKD
101 LYEYINPKTG IHSPMISKET YDIIMEHEDE LNSAIVYDRD FNYNYFGFKT
151 LERSYLLRIN GKVAERPQHL IMRVAVGIHG NDIPRVIETY NLMSQRFFTH
201 GSPCLFNAGT FRQMSSCFL LAMKDDSIEG IYDTLKSCAL ISKSAGGIGL
251 HIHNIRSTGA YIAGTNGTSN GIIPMVRVFN NTARYVDQGG NKRPGAFALY
301 LEPWHSDIFD FIDIRKNHGK EEIRARDLFP ALWIPDLFMK RVEQNGEWTL
351 FSPNEAPGLA DVYGDEFEEL YTKYEKENRG RQTIKAQKLW YAILGAQTET
401 GTPFMLYKDS CNRKSNQKNL GIIKSSNLCC EIVEYSAPDE VAVCNLASIA
451 LPSFVENDEK STYNFEKLH QVTKVVTRNL NRVIDRNHYP VPEAERSNMR
501 HRPIALGVQG LADAFMILRL PFDSQEAREL NIQIFETIYH AAVEASIELA
551 KEEGAYETYP GSPASQGLLQ FDLWNVKPTE LWDWDTLKQD LAKHGNRNSL
601 LVAPMPTAST SQILGNNECF EPYTSNIYSR RVLAGEFQIV NPYLLKDLVD
651 LGVWNDAMKS SIINNGSIQ ALPWIPDEIK ALYKTVWEIS QKHIIDMAAD
701 RAAFIDQSQS LNIHIKDPTN GKLTSMHFYG WKKGLKTGMY YLRTQAASAA
751 IQFTIDQKIA ETAGHIVRIL DELNIKKYVN KGRVEESENT DAPYKSFSTE
801 PTSLEESVAC LKIKDEGEKP RDDKTIEELE NDIYSAKVIA CAIDNPESCT
851 MCSC
```

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FIG. 15.

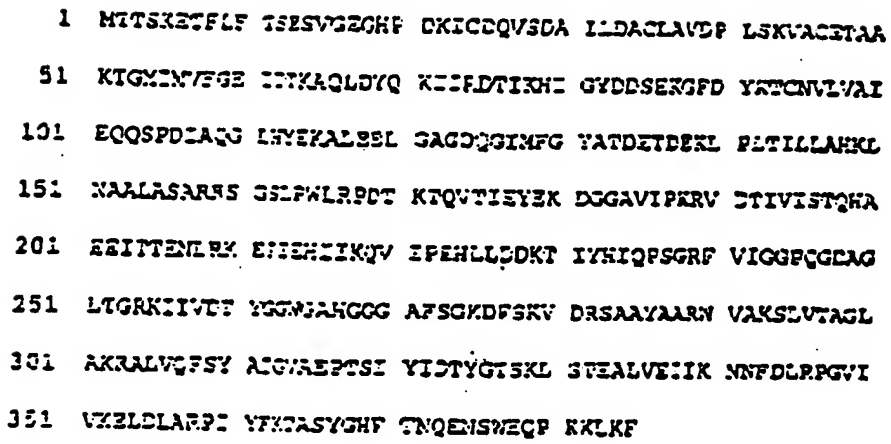
1 MTTSRETFLF TSESVGEGKP DKICDQVSDA ILDACLAVDP LSKVACETAA
51 KTGMIMVFGE ITTKAQLDYQ KIVRDTIKHI GYDDSEKGFD YKTCNVLVAI
101 EQQSPDIAQG VHYEKALEEL GAGDQGIMFG YATDETDELM PLTILLAHKL
151 NAALASARRS GSLPWLRPDT KTQVTIEYEK DGGAVIPKRV DTIVISTQHA
201 EEITTENLEK EIIEKIIKQV IPEHLLDDKT IYHIQPSGRF VIGGPQGDAG
251 LTGRKIIVDT YGGWGAHGGG AFSGKDPSKV DRSAAYAARW VAKSLVTAGL
301 AKRALVQFSY AIGVAEPTSI YIDTYGTSKL STEALVEIIK NNFDLRPGVI
351 VKELDLARPI YKQTASYGHF TNQEMSWEQP KKLKF

FIG. 16.

RH170498 AF101-AF150 (16 hours
glucose/maltose vs galactose/maltose
AF110

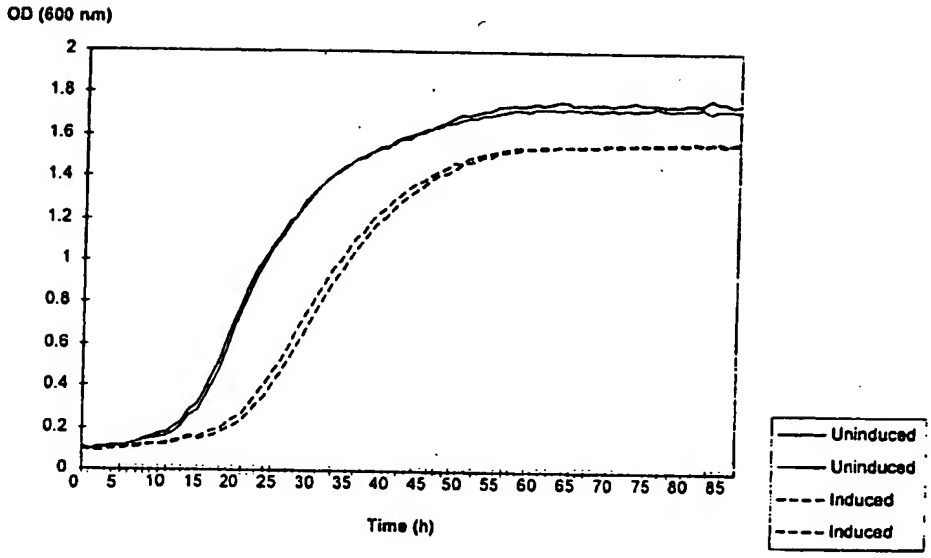

FIG. 17.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
genom. sample 113g

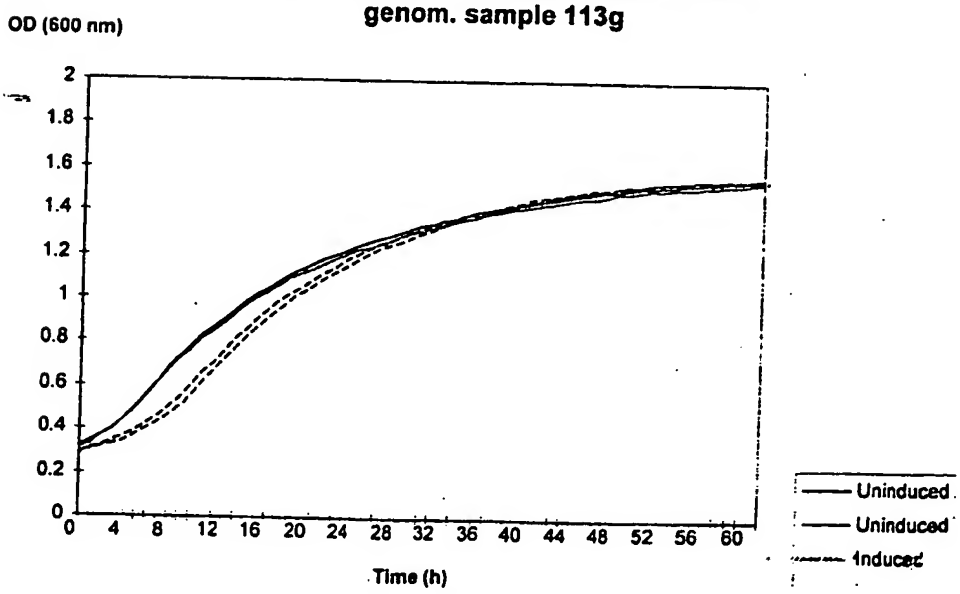

FIG. 18.

RH170498 AF101-AF150 (16 hours induction).
glucose/maltose vs galactose/maltose
AF117

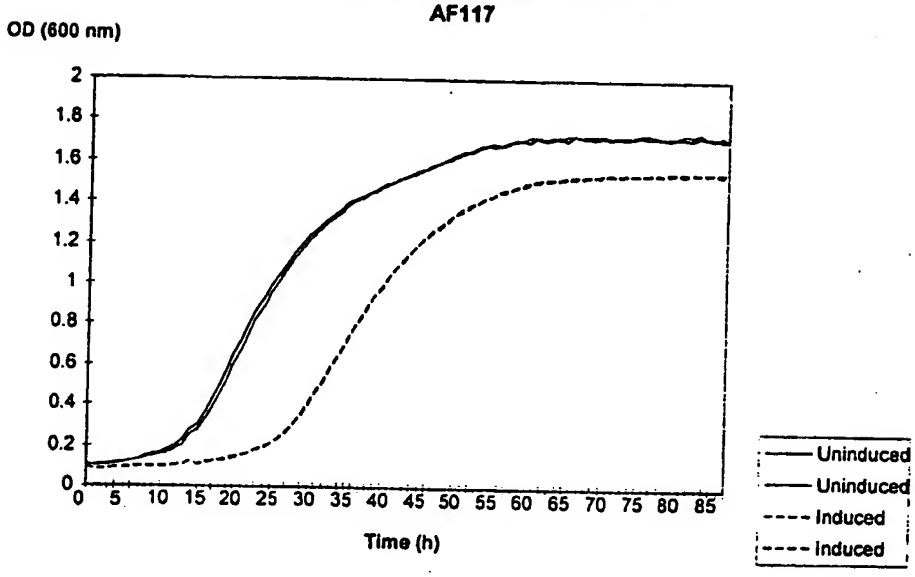

FIG. 19.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
genom. sample 135g

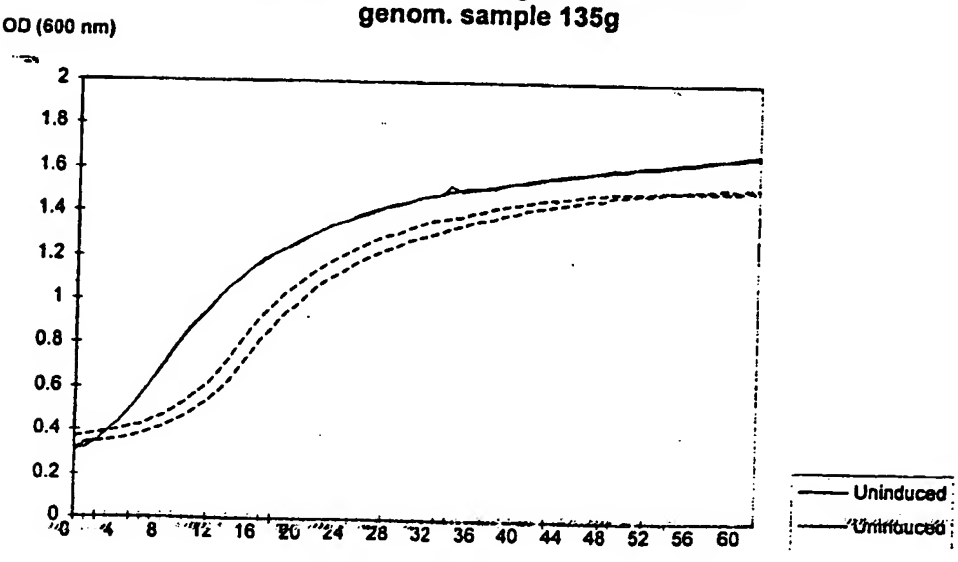

FIG. 20.

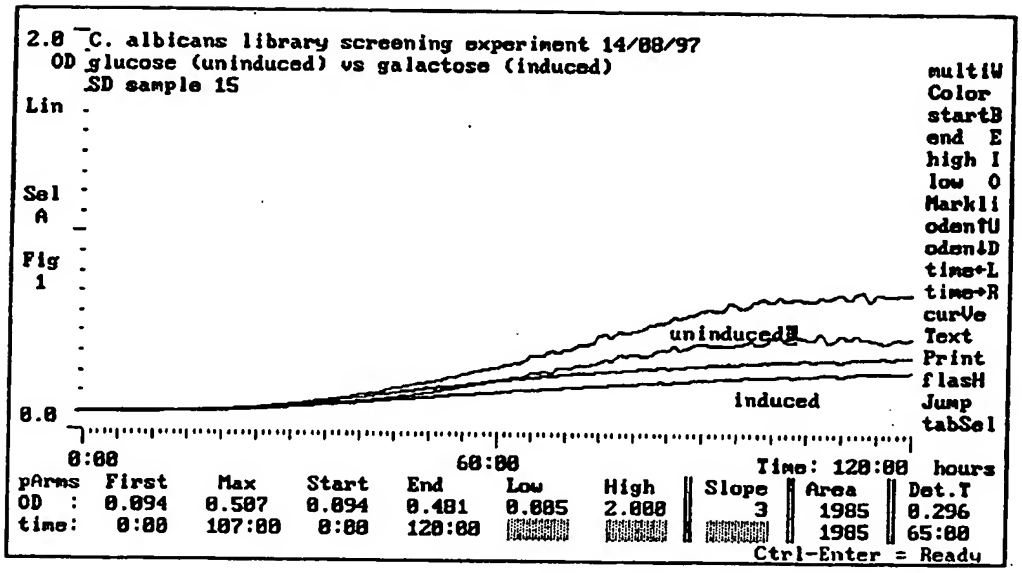
2.0 C. albicans library screening experiment 14/08/97
OD glucose (uninduced) vs galactose (induced)
SD sample 15
Lin
Sel A
Fig 1
0.0
uninduced
induced
0:00
60:00
Time: 120:00 hours
multiW
Color
startB
end E
high I
low O
MarkLi
odentU
odenLD
timeL
timeR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.094 0.507 0.094 0.481 0.005 2.000 3 1985 0.296
time: 0:00 107:00 0:00 120:00 1985 65:00
Ctrl-Enter = Ready

FIG. 21.

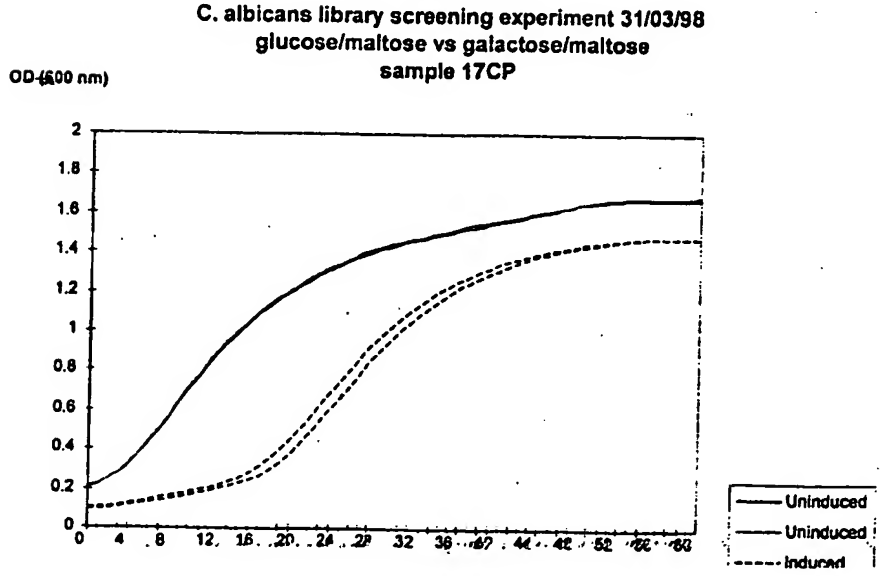
C. albicans library screening experiment 31/03/98
glucose/maltose vs galactose/maltose
sample 17CP
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 4 8 12 16 20 24 28 32 36 40 44 48 52 56 60
Uninduced
Uninduced
Induced

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FIG. 22.

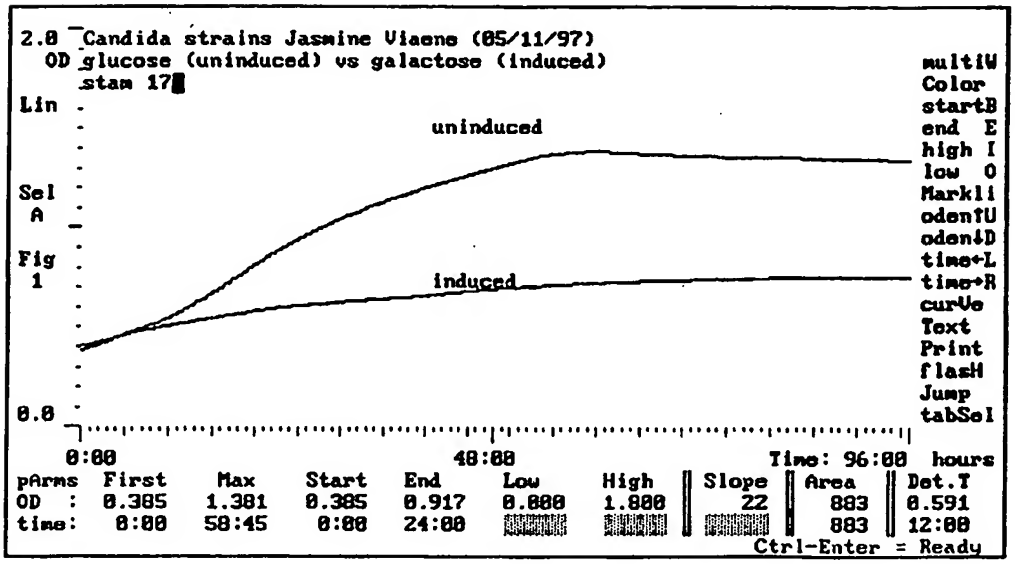

FIG. 23.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 190g

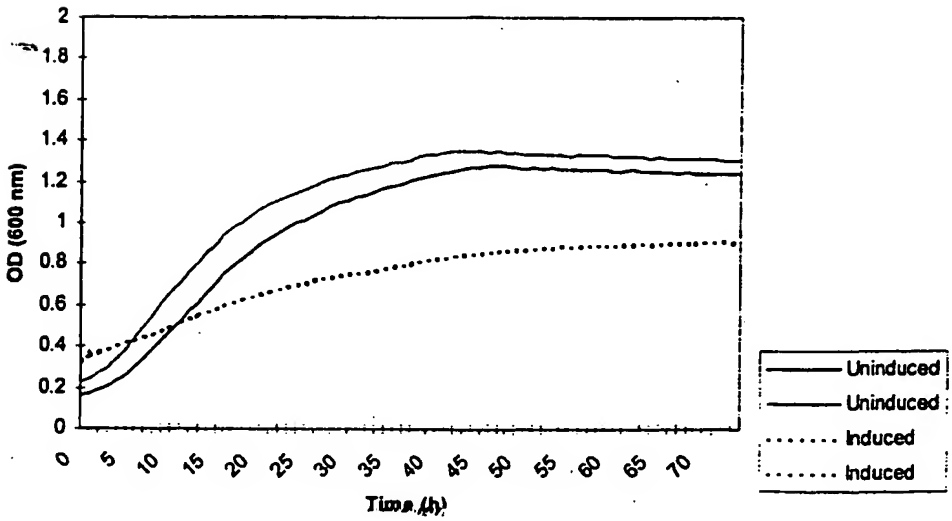

FIG. 24.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 207g

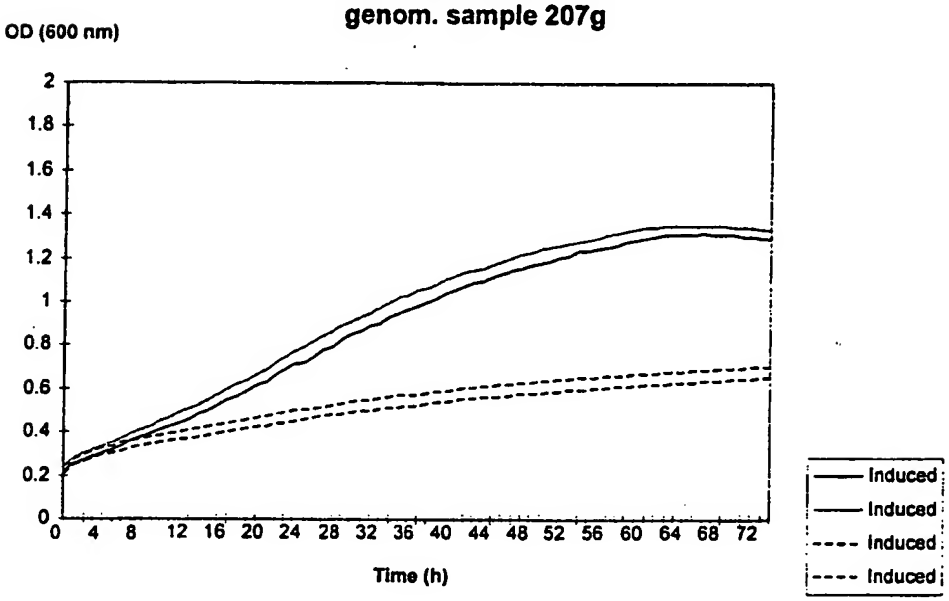

FIG. 25.

CP211-234+AF231-254 28/04/98 IVR
glucose/maltose vs galactose/maltose
sample CP214

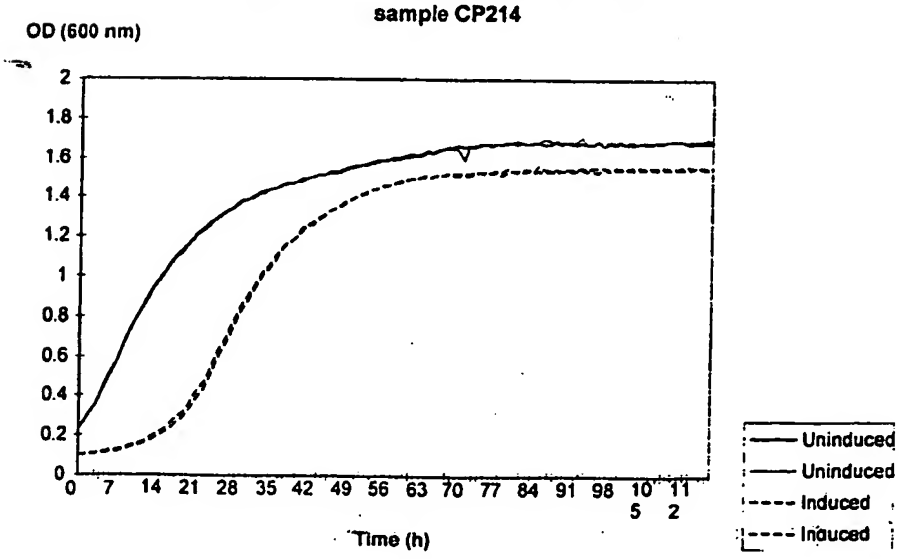

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FIG. 26.

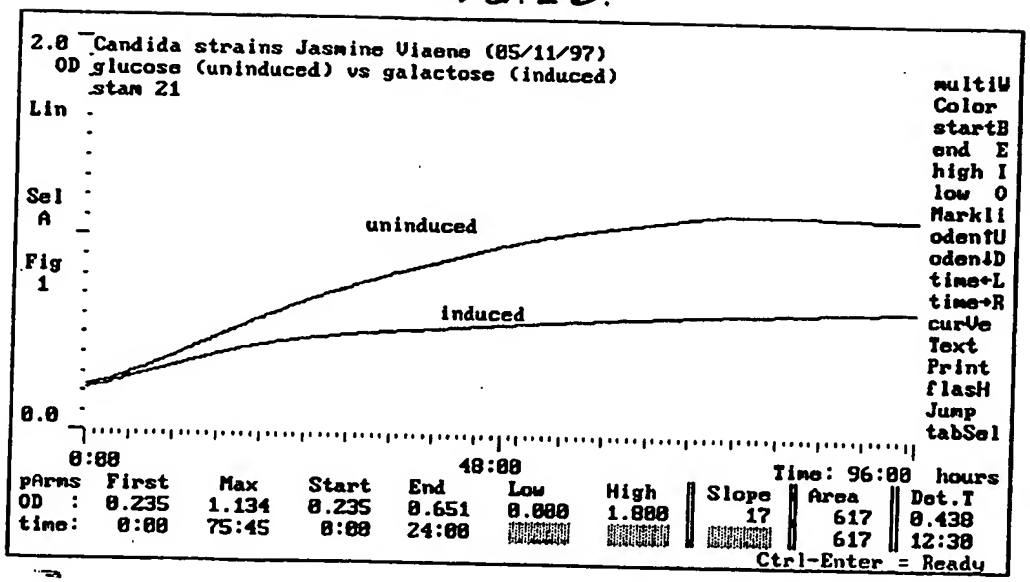
2.0
OD
Lin
Sel
A
Fig
1
0.0
Candida strains Jasmine Vlaene (05/11/97)
glucose (uninduced) vs galactose (induced)
stam 21
uninduced
induced
multiW
Color
startB
end E
high I
low 0
MarkLi
odenfU
odenfD
time+L
time+R
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.235 1.134 0.235 0.651 0.000 1.000 17 617 0.438
time: 0:00 75:45 0:00 24:00 617 12:30
Ctrl-Enter = Ready

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FIG. 27.

C. albicans library screening experiment 15/12/97
glucose vs galactose
genom. sample 222g

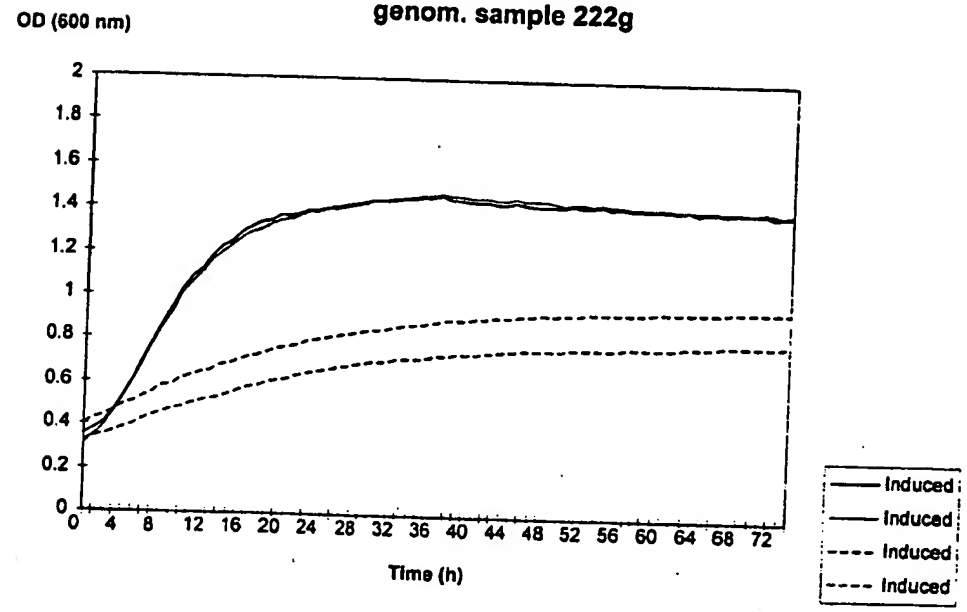

FIG. 28.

C. albicans library screening experiment 19/12/97
glucose/maltose vs galactose/maltose
genom. sample 222g

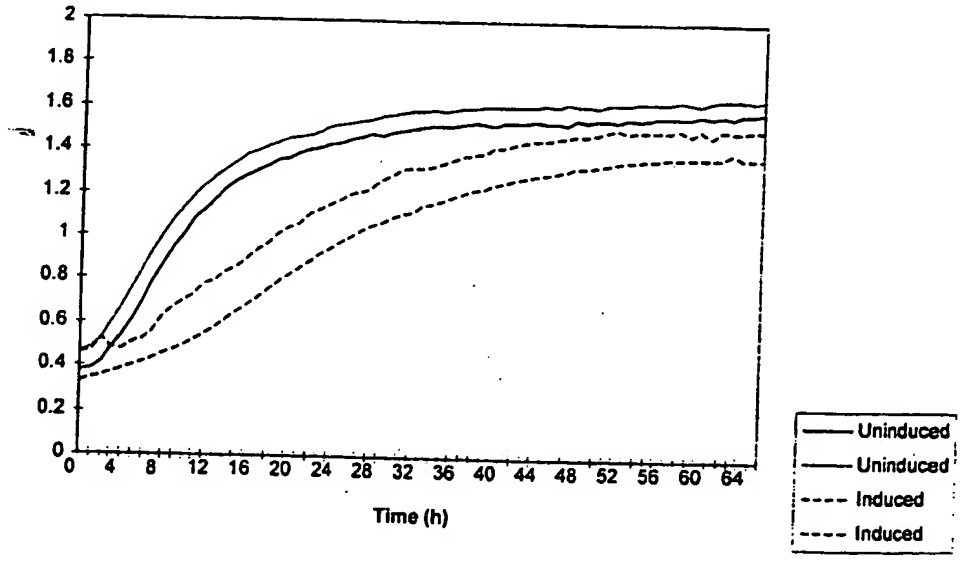

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FIG. 29.

CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP223

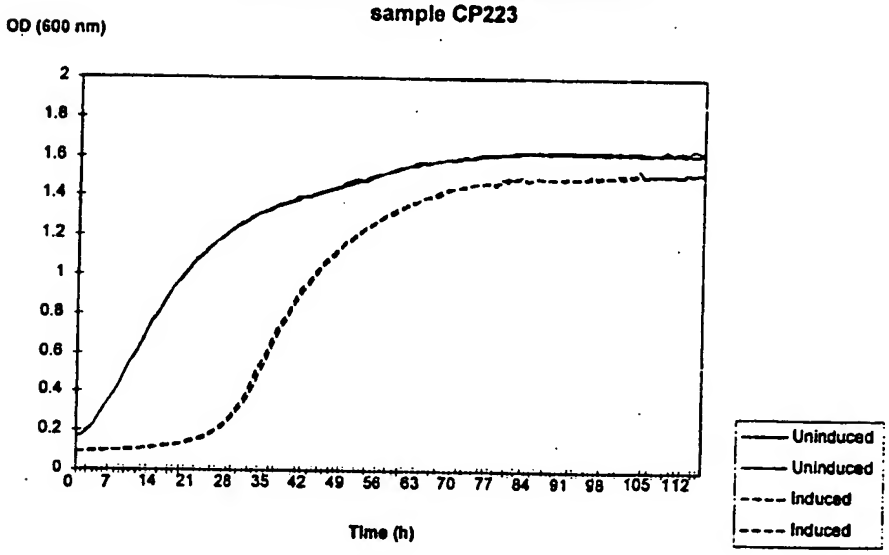

FIG. 30.

C. albicans library screening experiment 24/04/98
glucose/maltose vs galactose/maltose
sample 226af

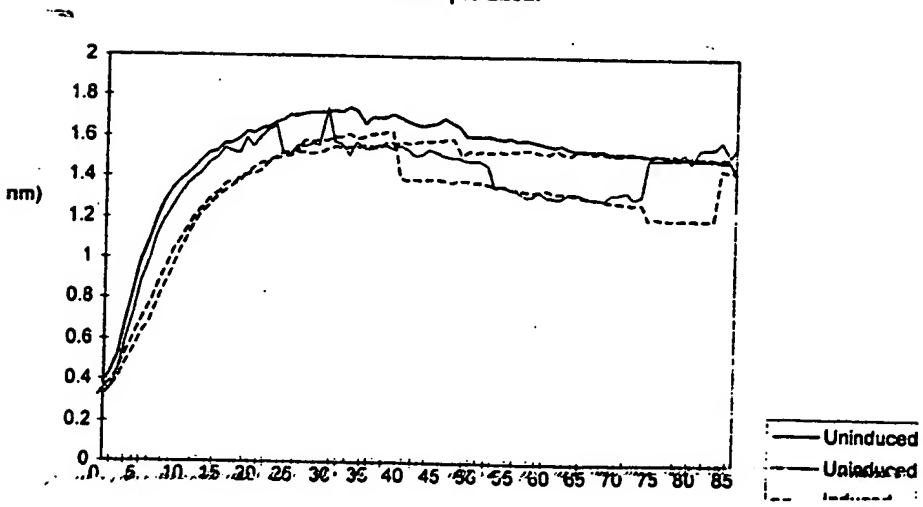

FIG. 31.

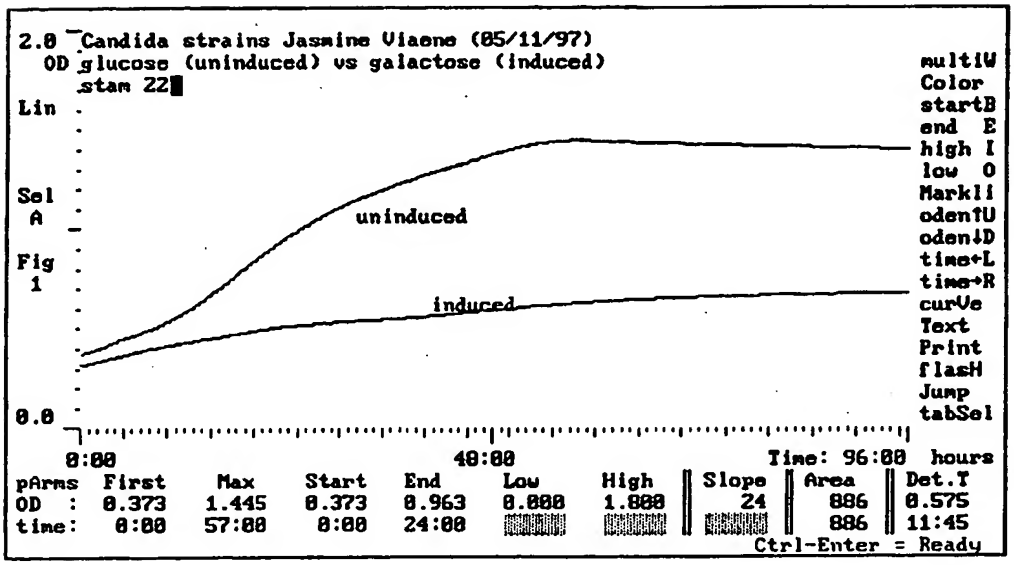
2.0
OD glucose (uninduced) vs galactose (induced)
Candida strains Jasmine Vlaene (05/11/97)
stam 22
Lin
Sel
A
Fig
1
uninduced
induced
0.0
0:00
40:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
MarkLi
odenTU
odenJD
timeL
timeR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.373 1.445 0.373 0.963 0.000 1.000 24 886 0.575
time: 0:00 57:00 0:00 24:00 886 11:45
Ctrl-Enter = Ready

FIG. 32.

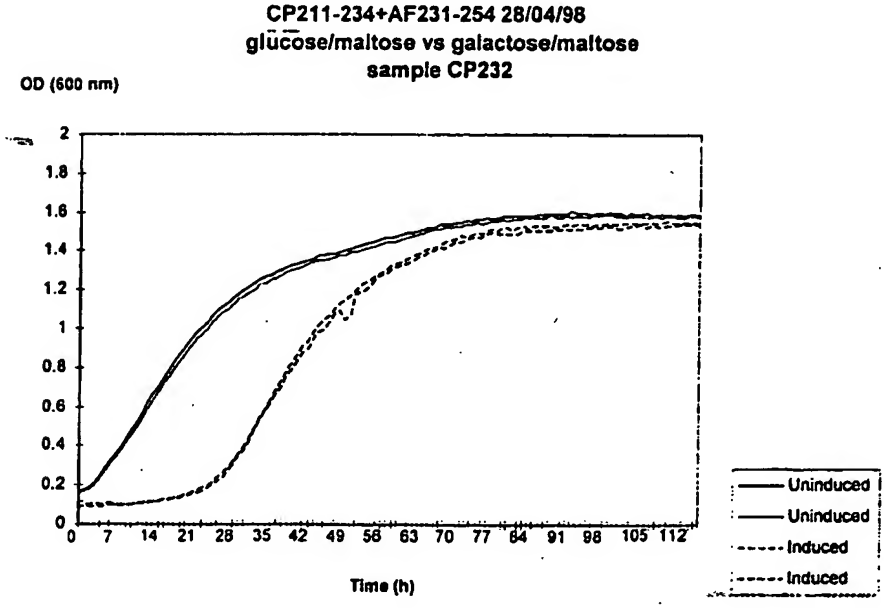
CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP232
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 7 14 21 28 35 42 49 56 63 70 77 84 91 98 105 112
Time (h)
Uninduced
Uninduced
Induced
Induced

FIG. 33.

CP211-234+AF231-254 28/04/98
glucose/maltose vs galactose/maltose
sample CP233

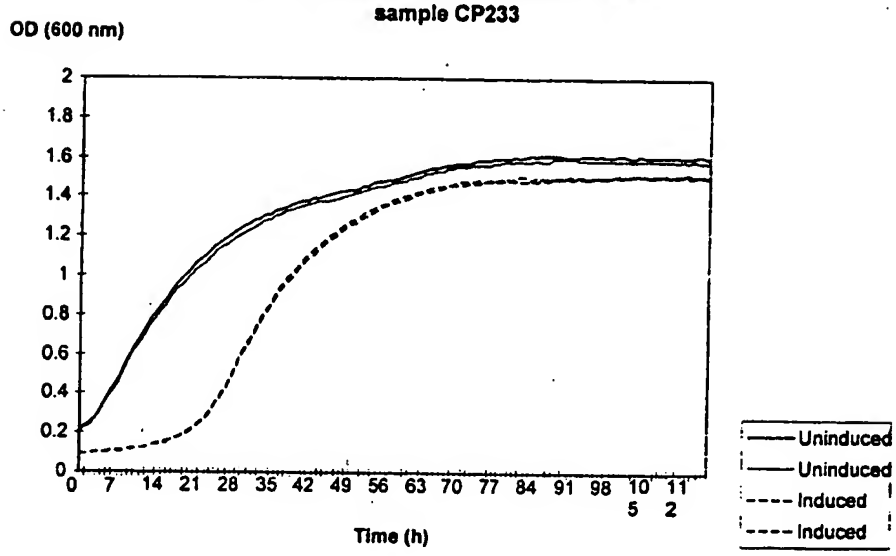

FIG. 34.

CP211-234+AF231-254 28/04/98 IVR
glucose/maltose vs galactose/maltose
sample AF249

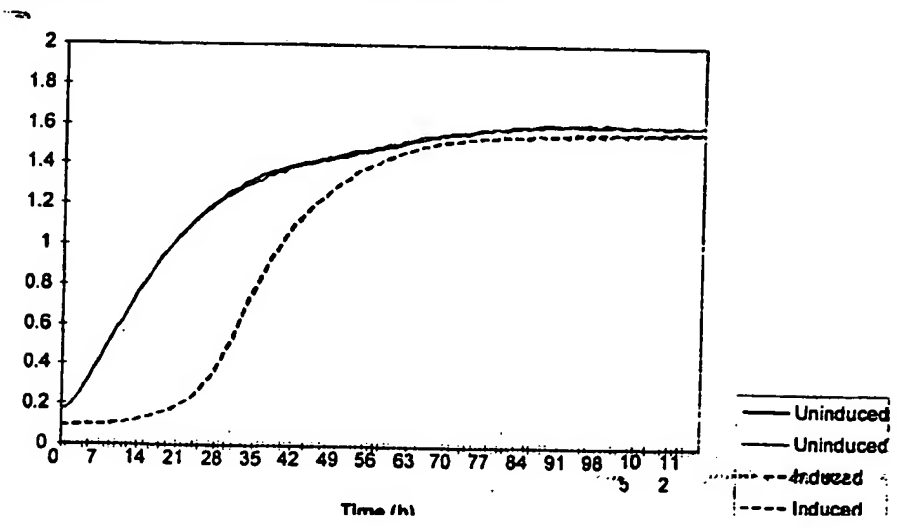

FIG. 35.

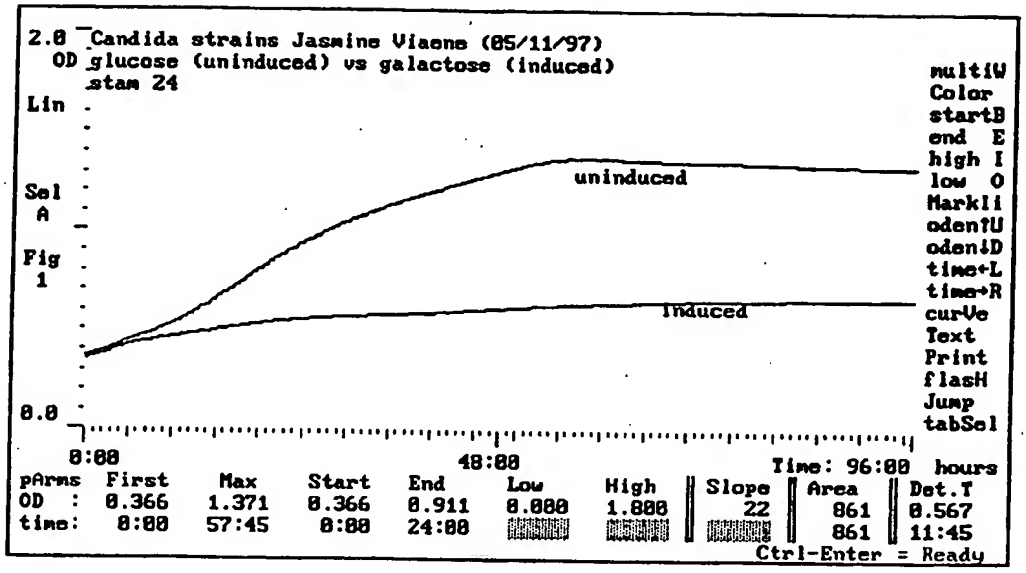
2.0 Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 24
Lin
Sel A
Fig 1
uninduced
induced
0.0
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
MarkLi
odenTU
odenJD
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.366 1.371 0.366 0.911 0.000 1.000 22 861 0.567
time: 0:00 57:45 0:00 24:00 861 11:45
Ctrl-Enter = Ready

FIG. 36.

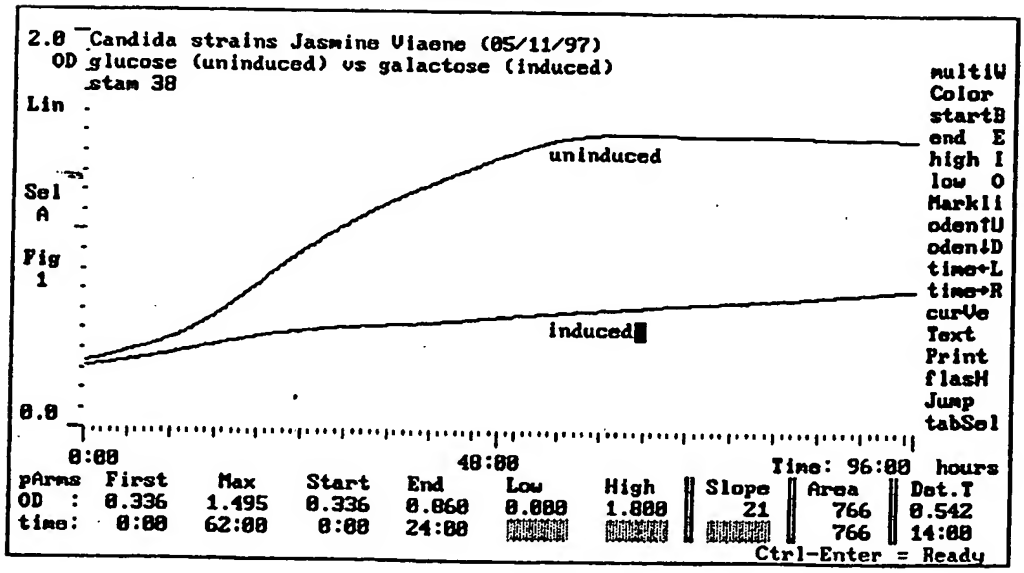
2.0 Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 38
Lin
Sel A
Fig 1
uninduced
induced
0.0
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
MarkLi
odenTU
odenJD
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.336 1.495 0.336 0.860 0.000 1.000 21 766 0.542
time: 0:00 62:00 0:00 24:00 766 14:00
Ctrl-Enter = Ready

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FIG. 37.

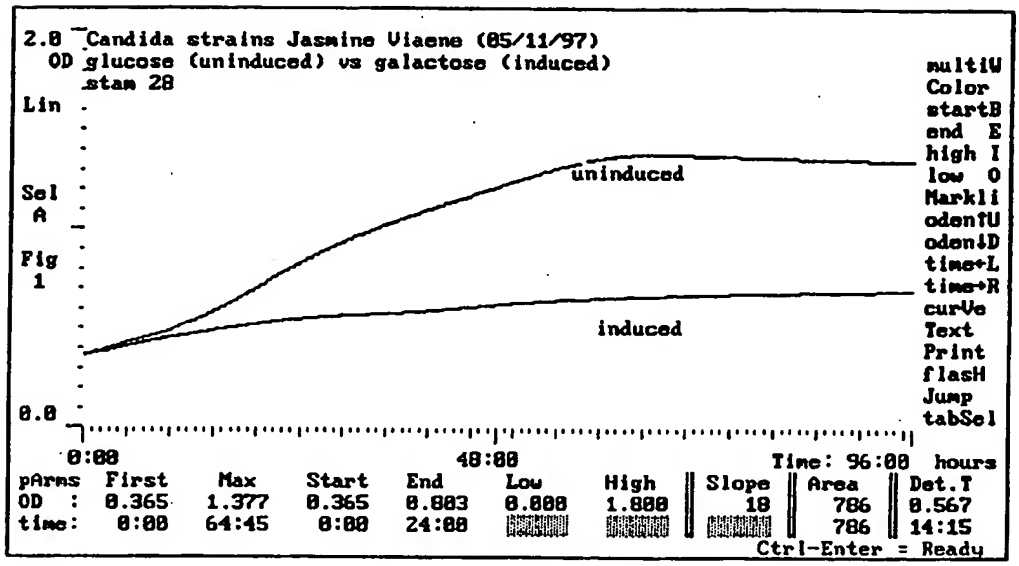

FIG. 38.

C. albicans library screening experiment 27/10/97
glucose vs galactose
YPD sample 328

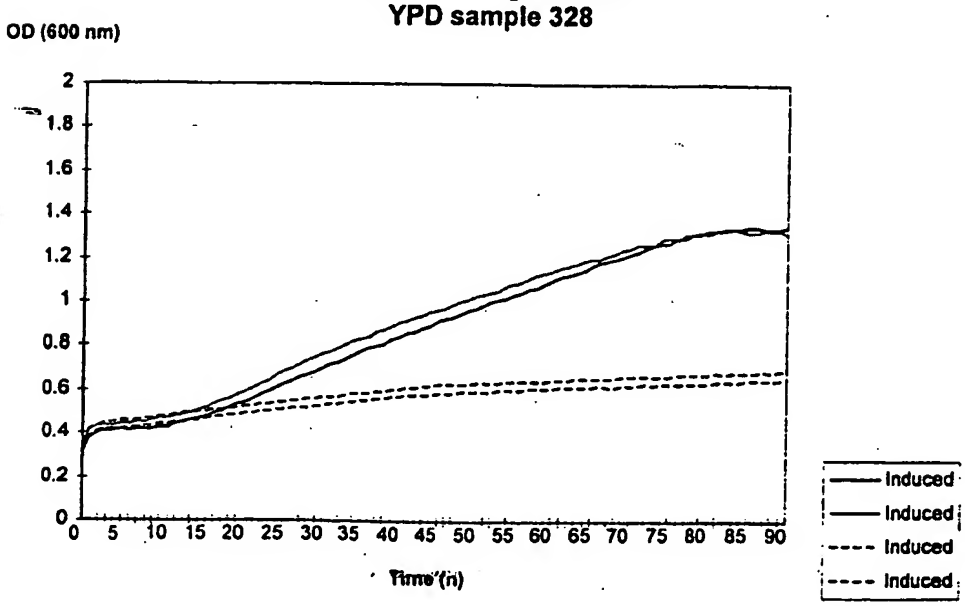

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FIG. 39

C. albicans cDNA library screening 12-02-98
glucose/maltose vs galactose/maltose
YPD sample 357

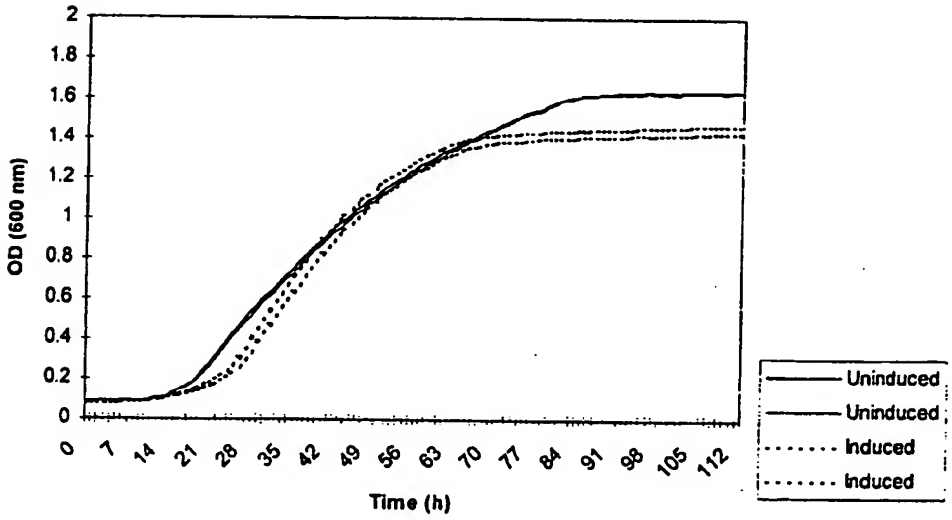

FIG. 40

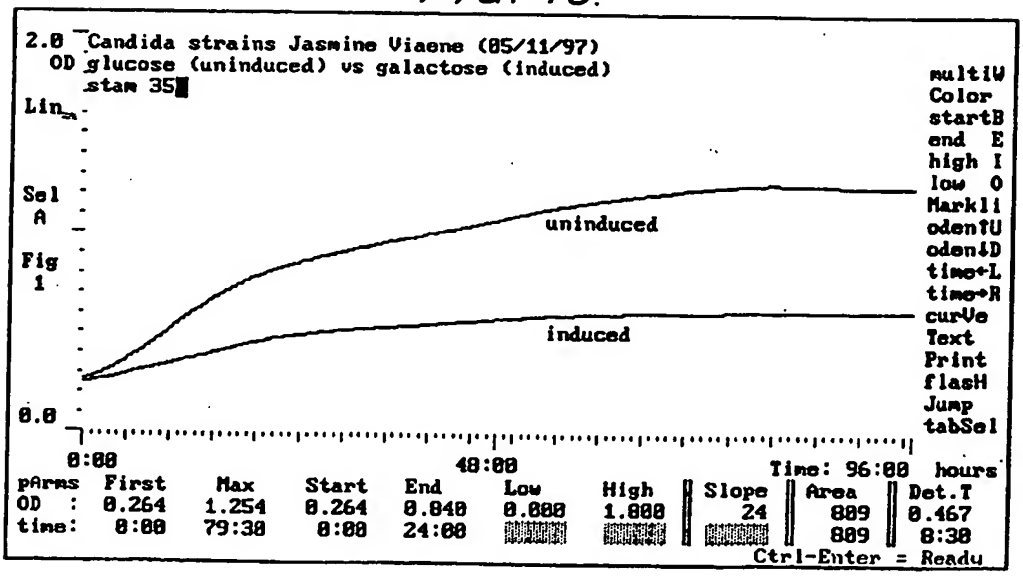

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FIG. 41.

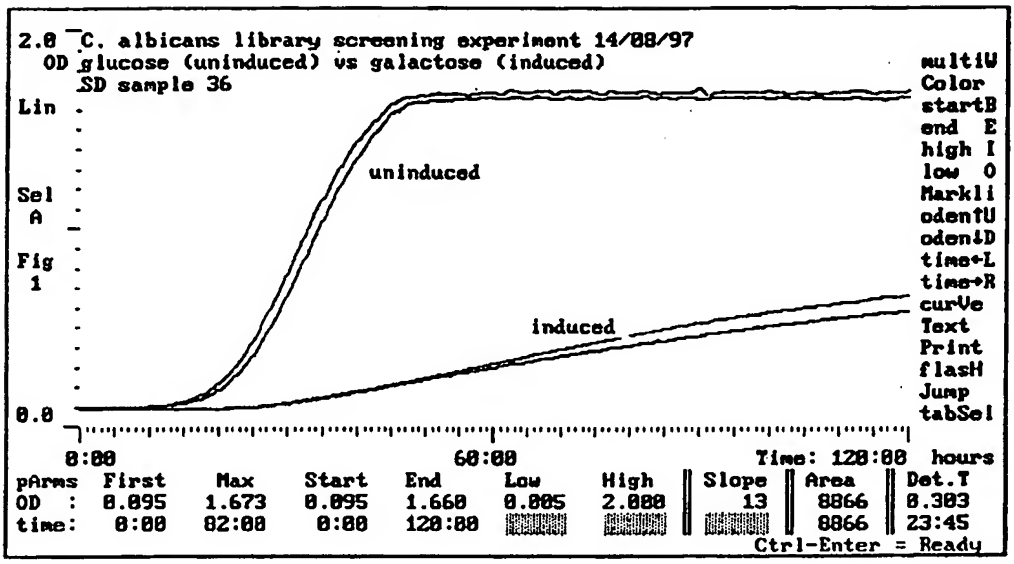

FIG. 42.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
sample 36 (SAM2)

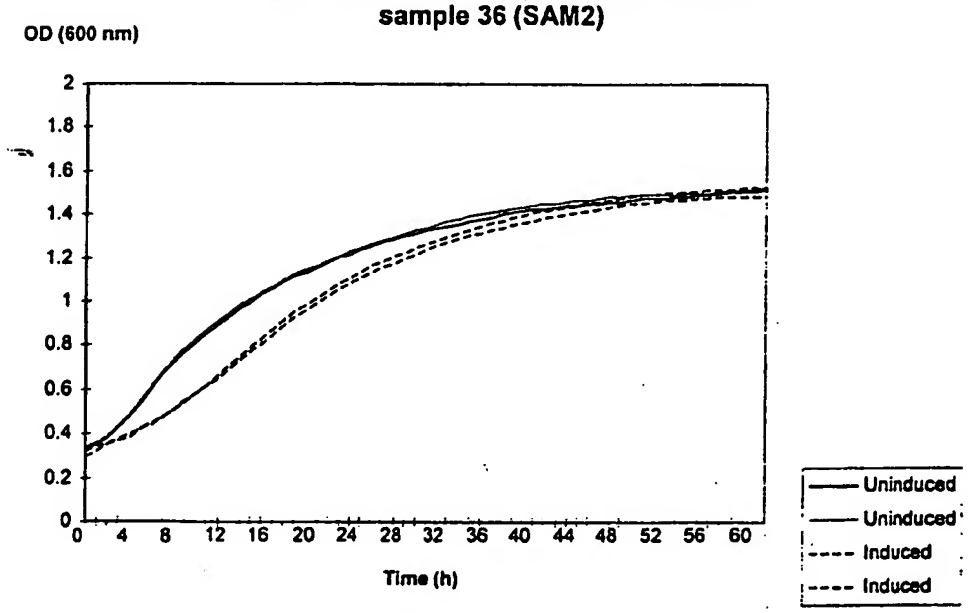

FIG. 43.

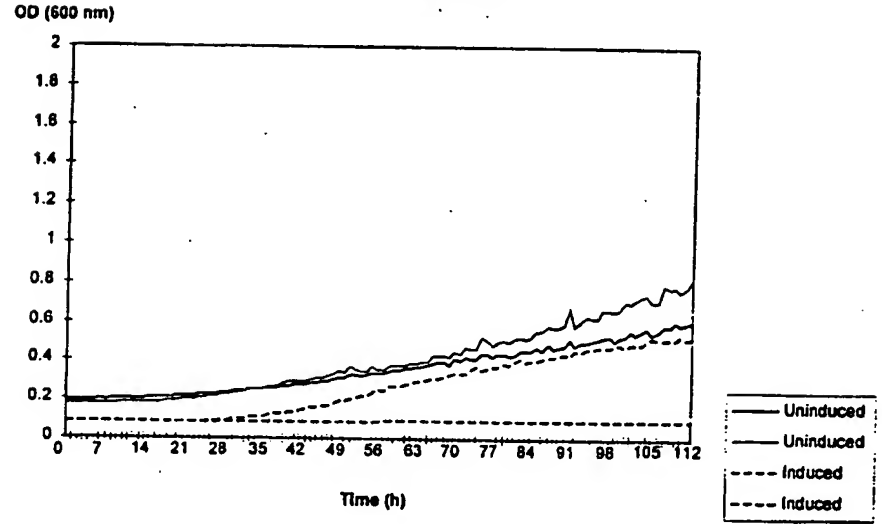
C. albicans cDNA library screening 05/02/98
glucose/maltose vs galactose/maltose
YPD sample 360
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 7 14 21 28 35 42 49 56 63 70 77 84 91 98 105 112
Time (h)
Uninduced
Uninduced
Induced
Induced

FIG. 44.

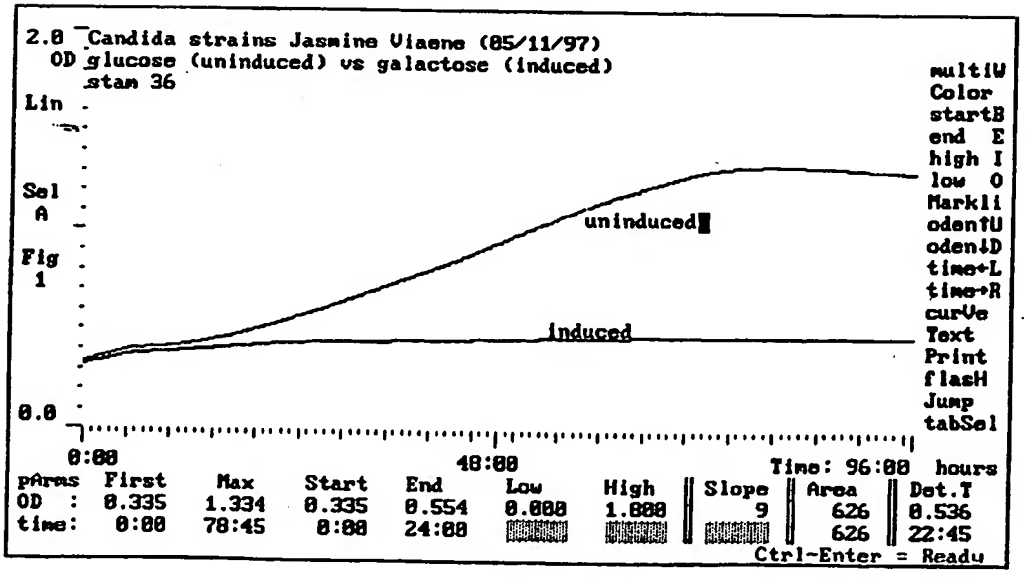
2.0
Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 36
Lin
Sel
A
Fig
1
uninduced
induced
0.0
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenTU
odenJD
time←L
time→R
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.335 1.334 0.335 0.554 0.000 1.000 9 626 0.536
time: 0:00 78:45 0:00 24:00 626 22:45
Ctrl-Enter = Readu

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FIG. 45.

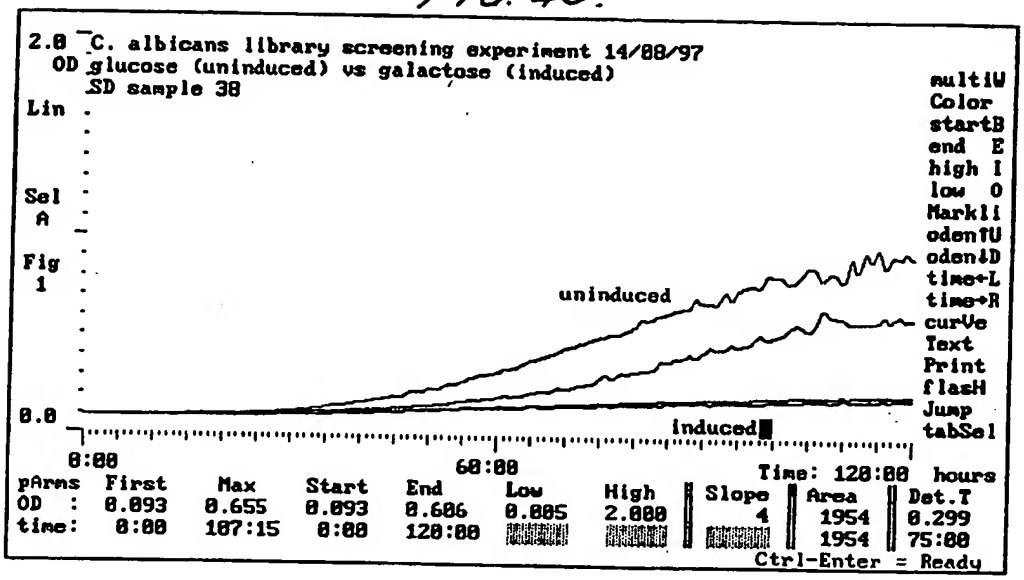


FIG. 46.

C. albicans library screening experiment 28/11/97
glucose/maltose vs galactose/maltose
sample 38 (RNR)

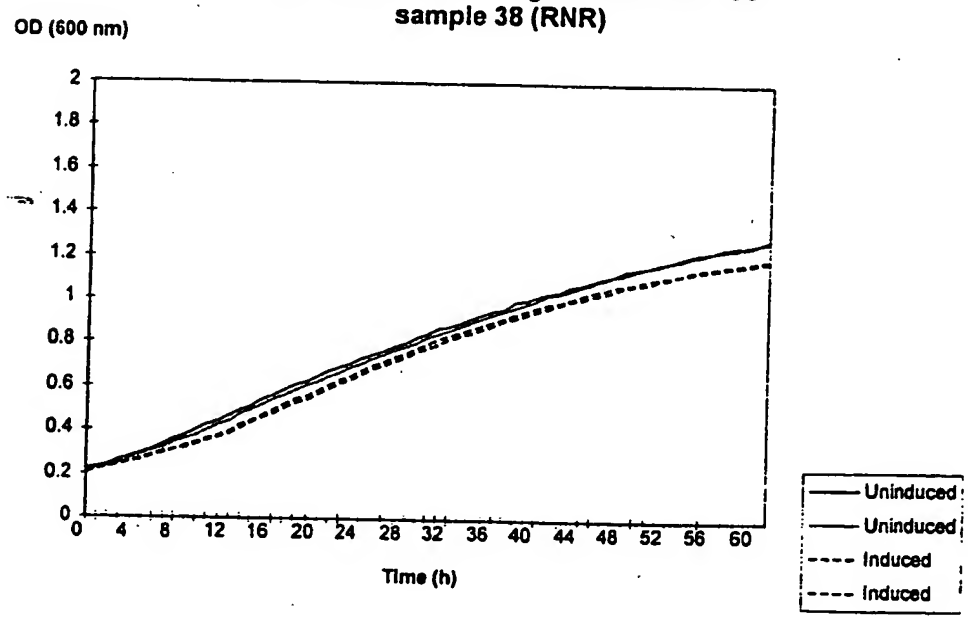
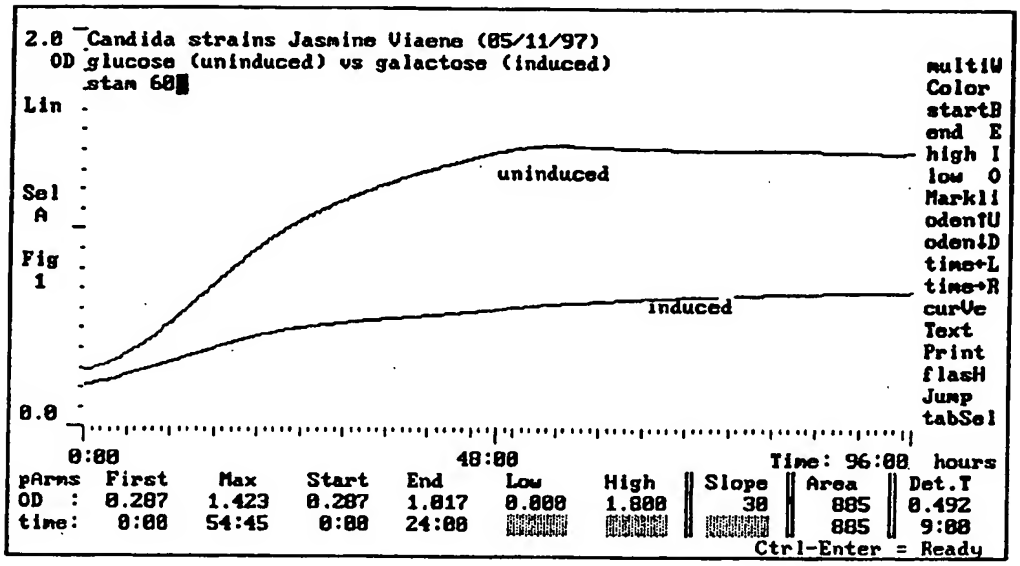


FIG. 47.



60gK (RAD18)

FIG. 48.

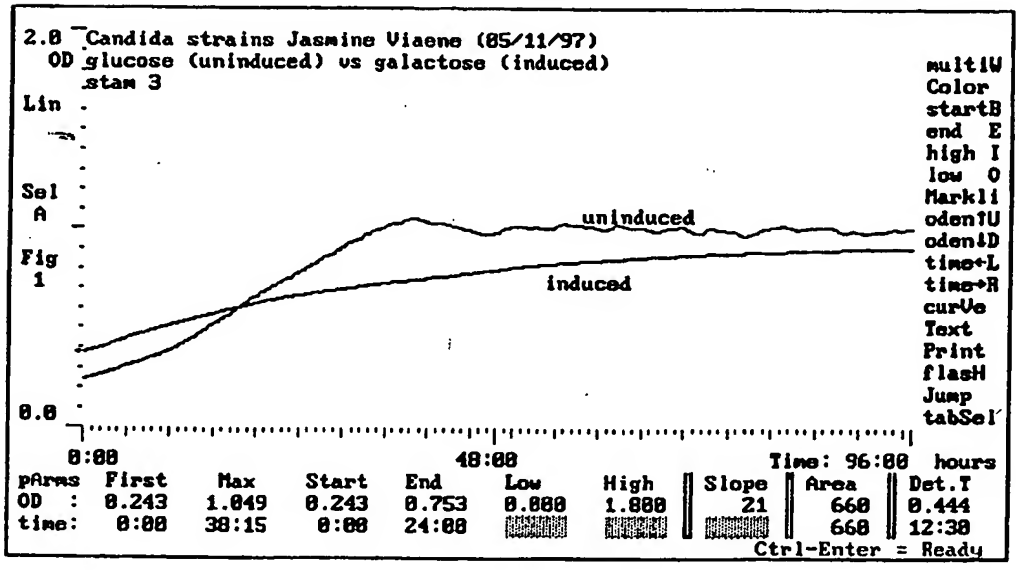


FIG. 49.

C. albicans cDNA library screening 12-02-98
glucose/maltose vs galactose/maltose
YPD sample 409

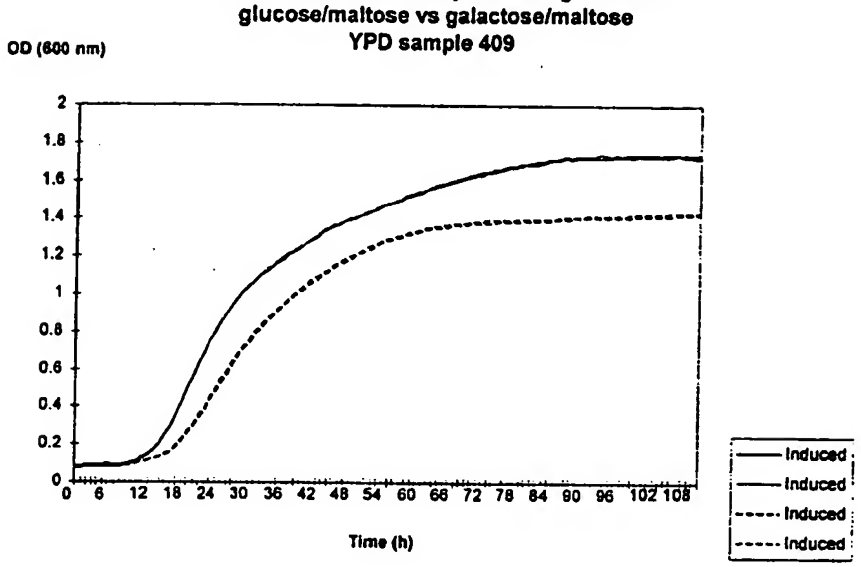


FIG. 50.

C. albicans library screening experiment 27/03/98
glucose/maltose vs galactose/maltose
sample 40AF

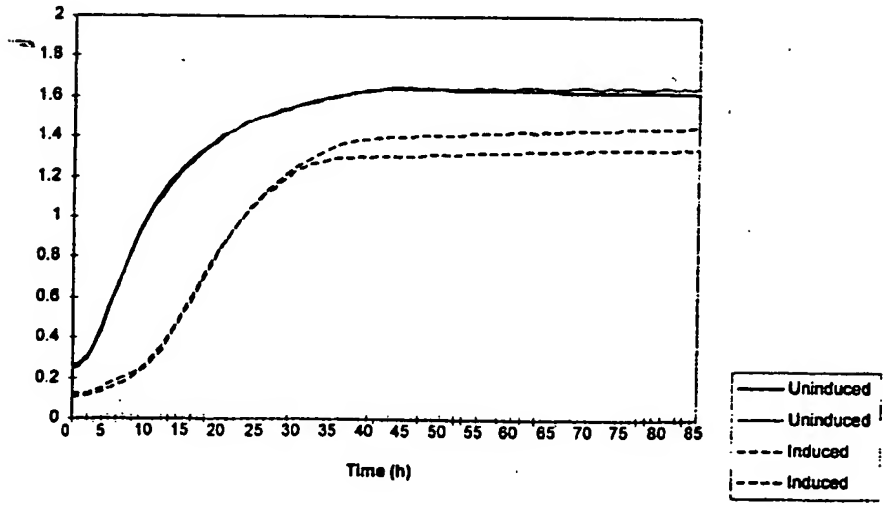


FIG. 51.

C. albicans library screening experiment 17/03/98
glucose/maltose vs galactose/maltose
SD sample 485c

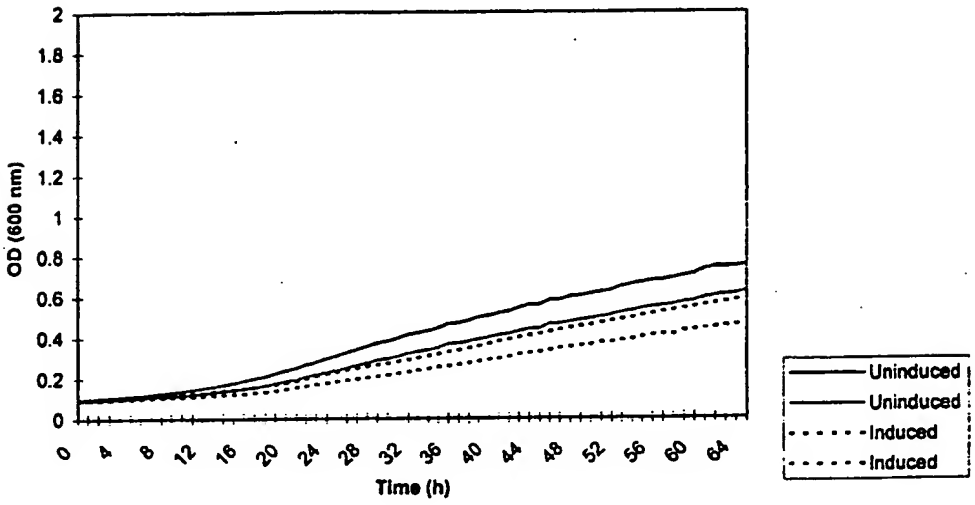


FIG. 52.

C. albicans cDNA library screening 10-03-98
glucose vs galactose
SD sample 480c

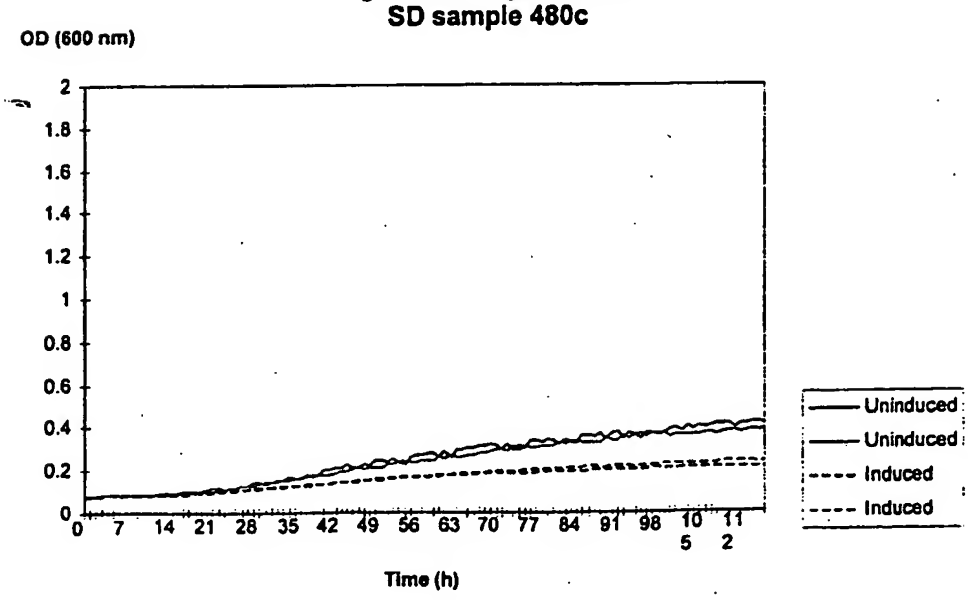


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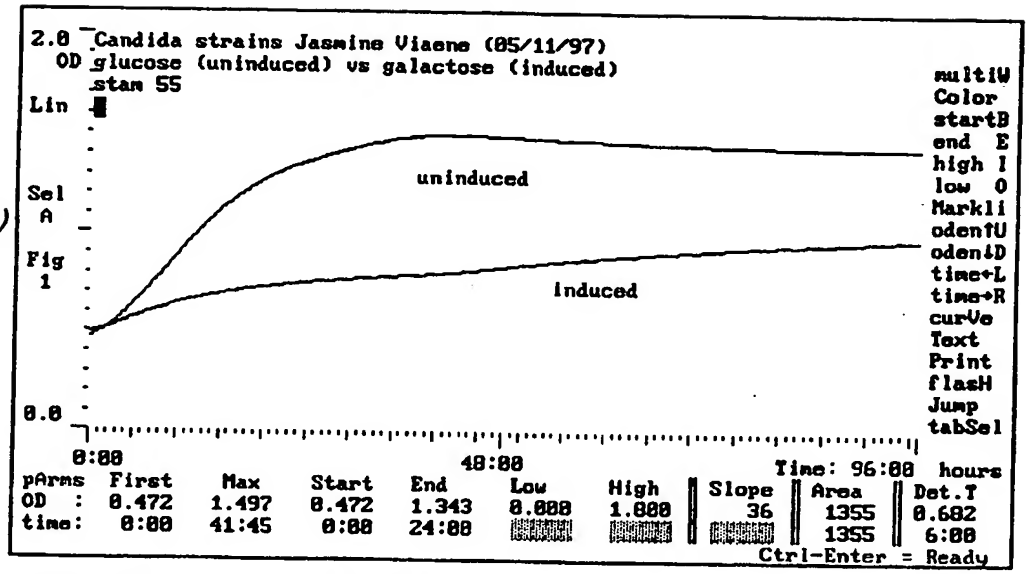
FIG.53.


(a)
2.0 Candida strains Jasmine Viaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stan 55
Lin
Sel A
Fig 1
uninduced
induced
0.0
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.472 1.497 0.472 1.343 0.000 1.000 36 1355 0.682
time: 0:00 41:45 0:00 24:00 1355 6:00
Ctrl-Enter = Ready
multiW
Color
startB
end E
high I
low O
MarkLi
odenTU
odenLD
time+L
time+R
curVe
Text
Print
flasH
Jump
tabSel

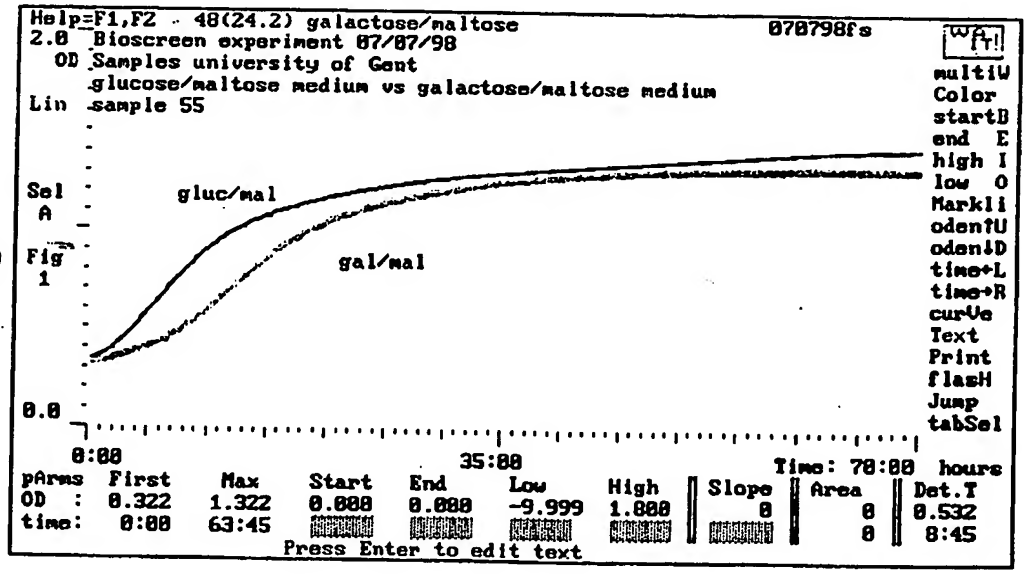

(b)
Help=F1,F2 - 48(24.2) galactose/maltose
070798fs
2.0 Bioscreen experiment 07/07/98
OD Samples university of Gent
glucose/maltose medium vs galactose/maltose medium
Lin sample 55
Sel A
Fig 1
gluc/mal
gal/mal
0.0
0:00
35:00
Time: 78:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.322 1.322 0.000 0.000 -9.999 1.000 0 0 0.532
time: 0:00 63:45 0 0 8:45
Press Enter to edit text
multiW
Color
startB
end E
high I
low O
MarkLi
odenTU
odenLD
time+L
time+R
curVe
Text
Print
flasH
Jump
tabSel

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FIG. 54

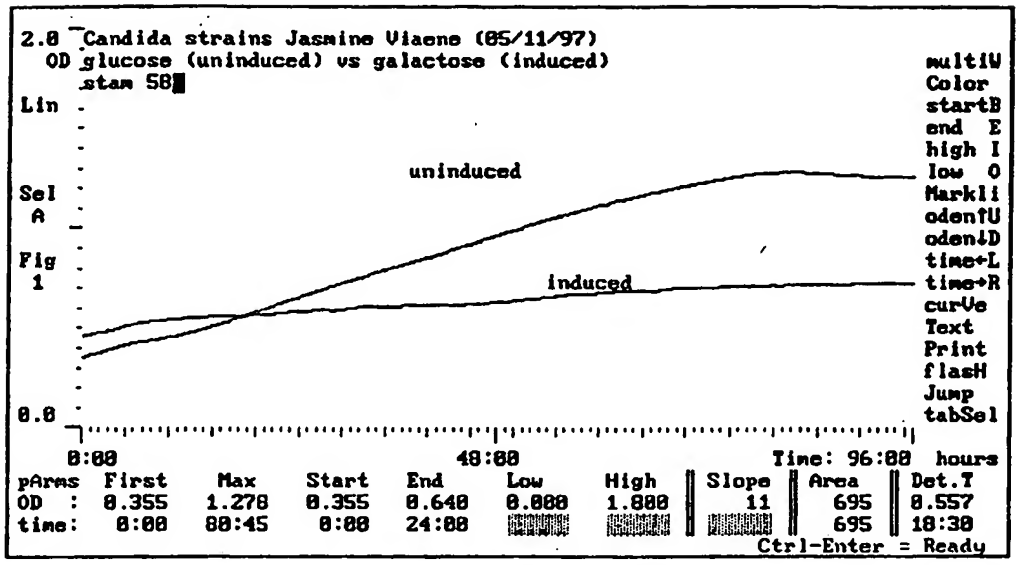

FIG. 55.

C. albicans library screening experiment 31/03/98
glucose/maltose vs galactose/maltose
sample 8CP

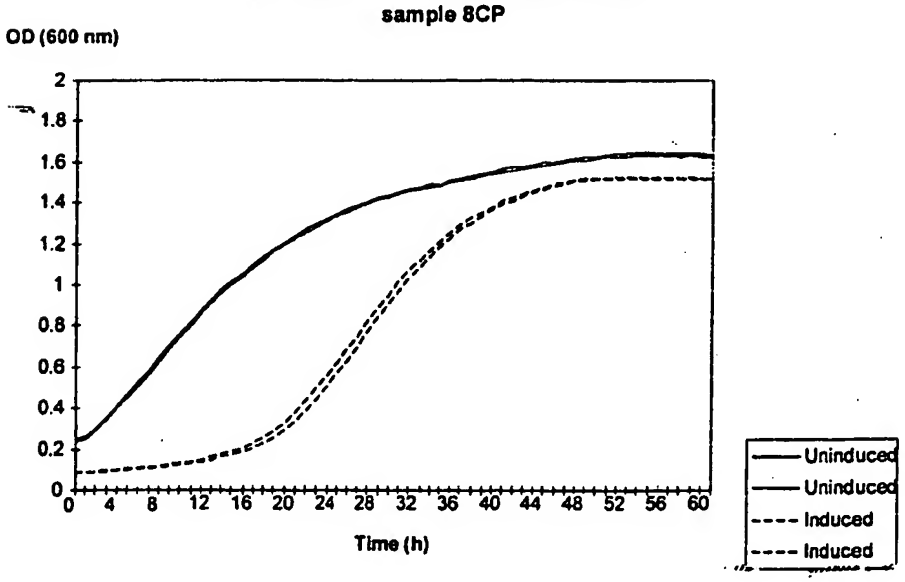

FIG. 56.

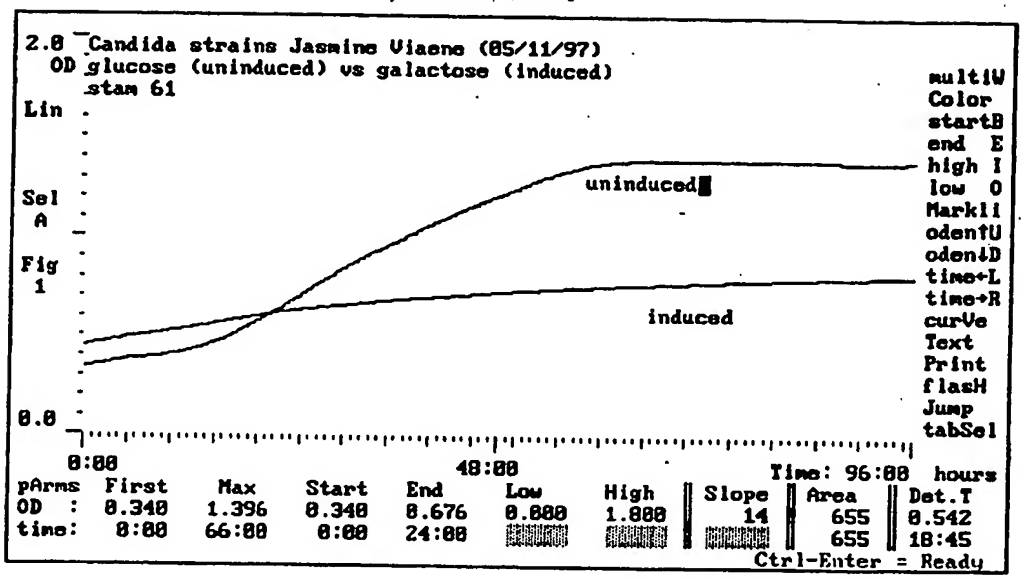
2.0
Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 61
Lin
Sel
A
Fig
1
0.0
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenfU
odenfD
time+L
time+R
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.340 1.396 0.340 0.676 0.000 1.000 14 655 0.542
time: 0:00 66:00 0:00 24:00 655 18:45
Ctrl-Enter = Ready

FIG. 57.

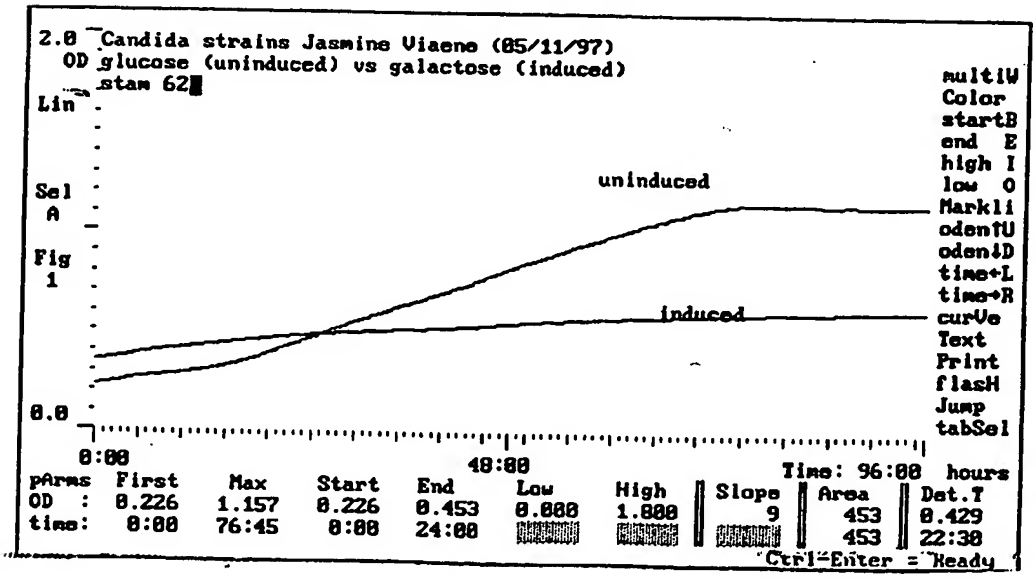
2.0
Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 62
Lin
Sel
A
Fig
1
0.0
uninduced
induced
multiW
Color
startB
end E
high I
low O
Markli
odenfU
odenfD
time+L
time+R
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.226 1.157 0.226 0.453 0.000 1.000 9 453 0.429
time: 0:00 76:45 0:00 24:00 453 22:30
Ctrl-Enter = Ready

FIG. 58.

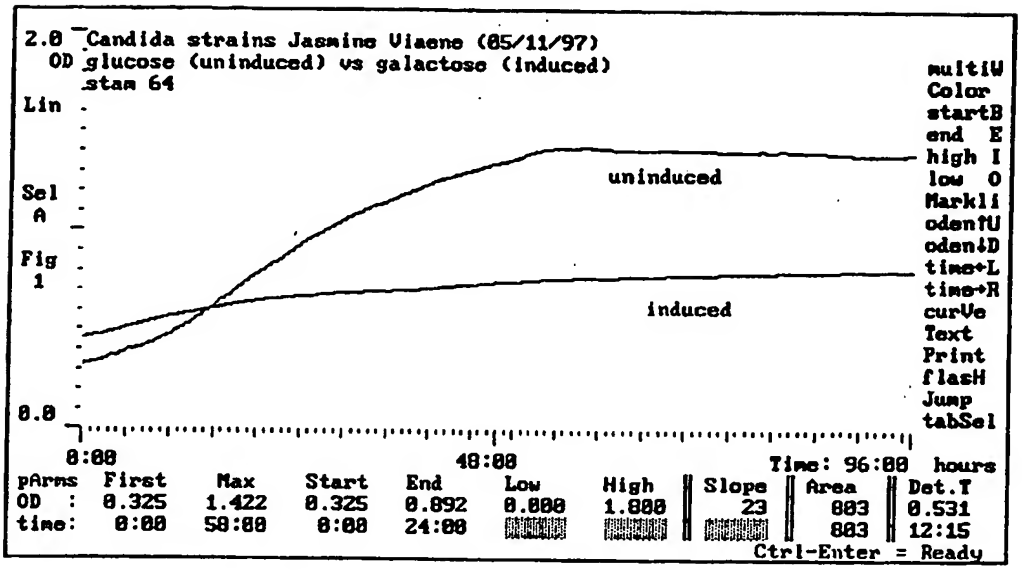
2.0
Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 64
Lin
Sel
A
Fig
1
0.0
uninduced
induced
multiV
Color
startB
end E
high I
low O
MarkLi
odenfU
odenfD
time+L
time+R
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.325 1.422 0.325 0.892 0.000 1.000 23 883 0.531
time: 0:00 58:00 0:00 24:00 883 12:15
Ctrl-Enter = Ready

FIG. 59.

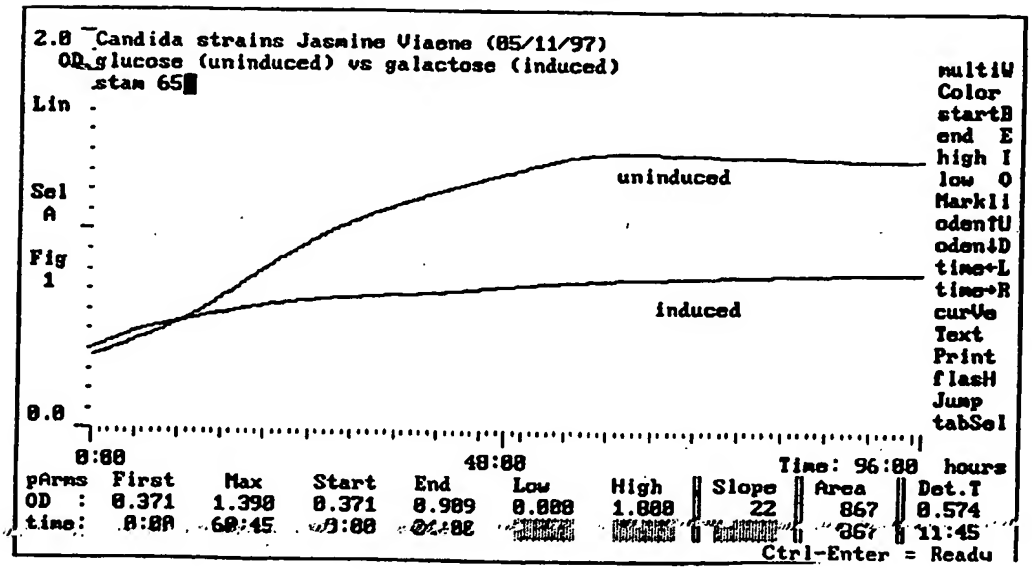
2.0
Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 65
Lin
Sel
A
Fig
1
0.0
uninduced
induced
multiV
Color
startB
end E
high I
low O
MarkLi
odenfU
odenfD
time+L
time+R
curVe
Text
Print
flasH
Jump
tabSel
0:00
48:00
Time: 96:00 hours
pArms First Max Start End Low High Slope Area Det.T
OD : 0.371 1.390 0.371 0.989 0.000 1.000 22 867 0.574
time: 0:00 60:45 0:00 24:00 867 11:45
Ctrl-Enter = Ready

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FIG. 60.

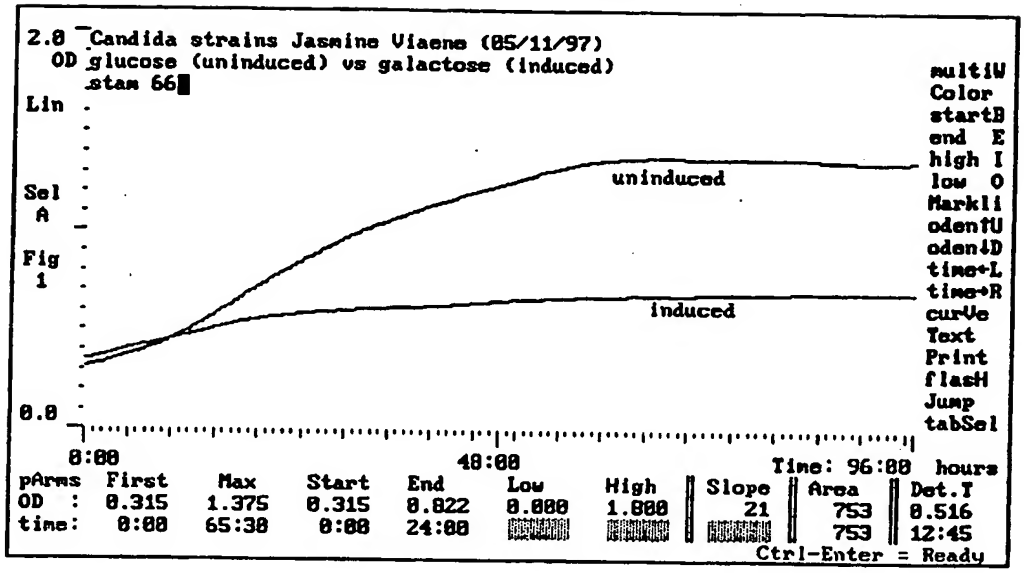


FIG. 61.

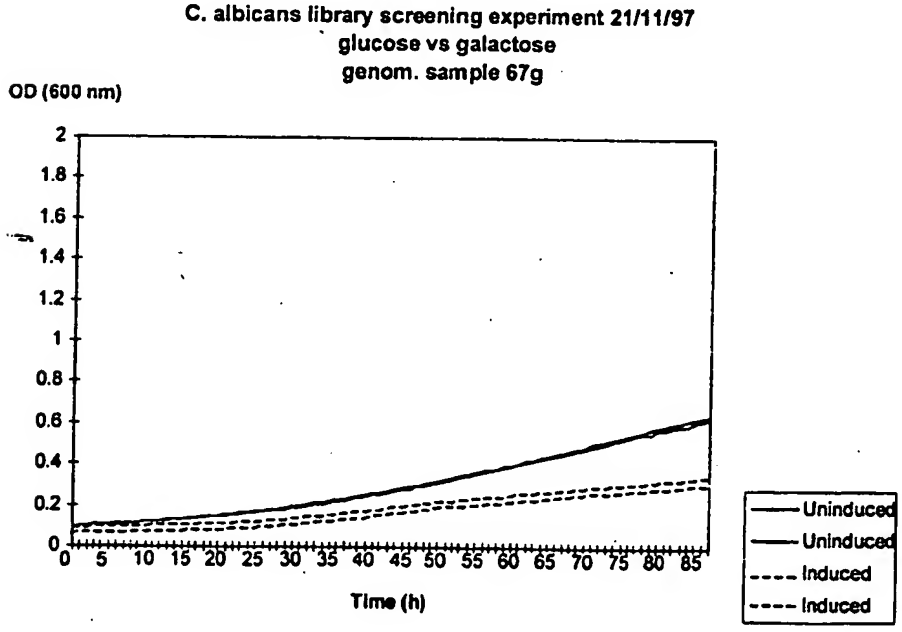


FIG. 62.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 80g

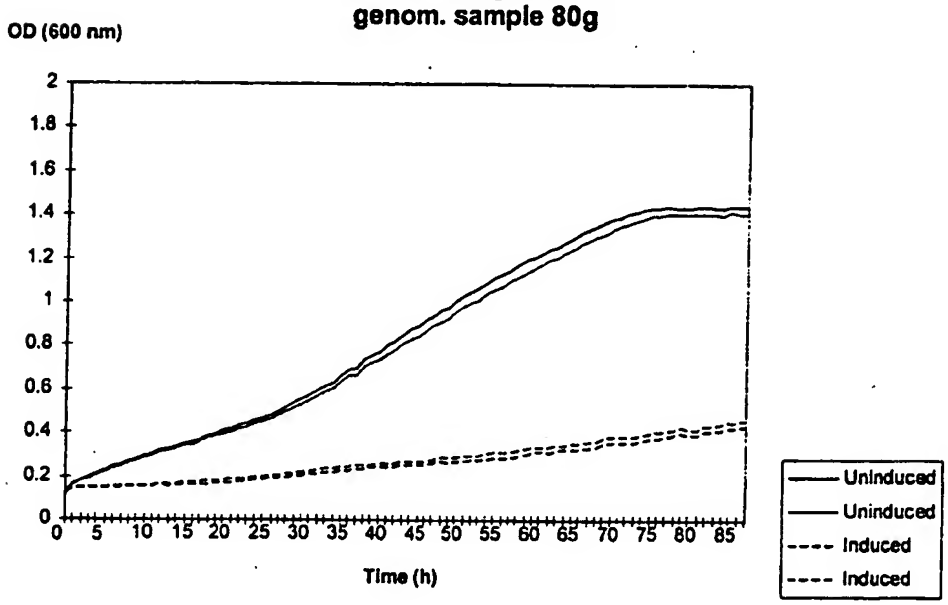
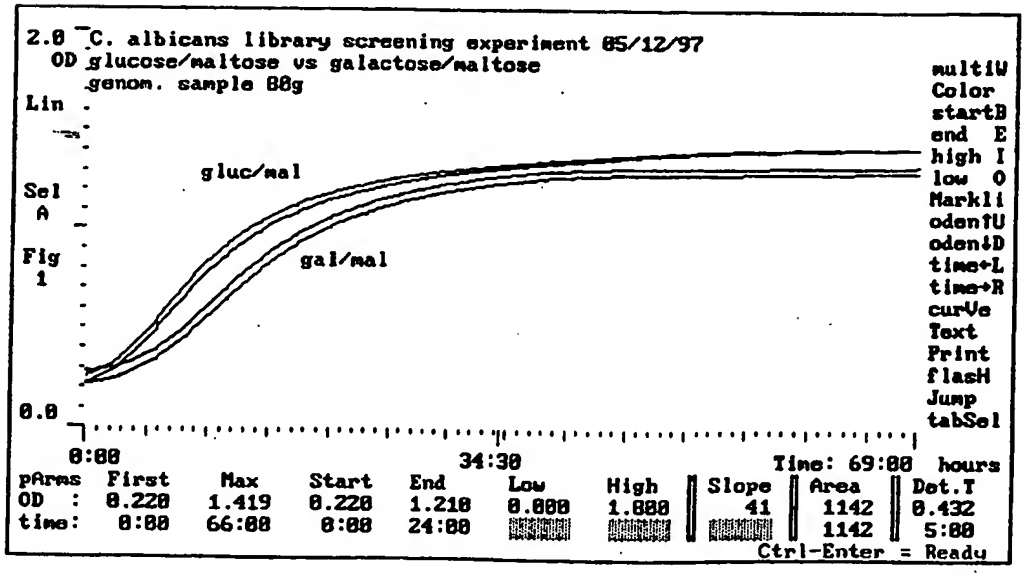
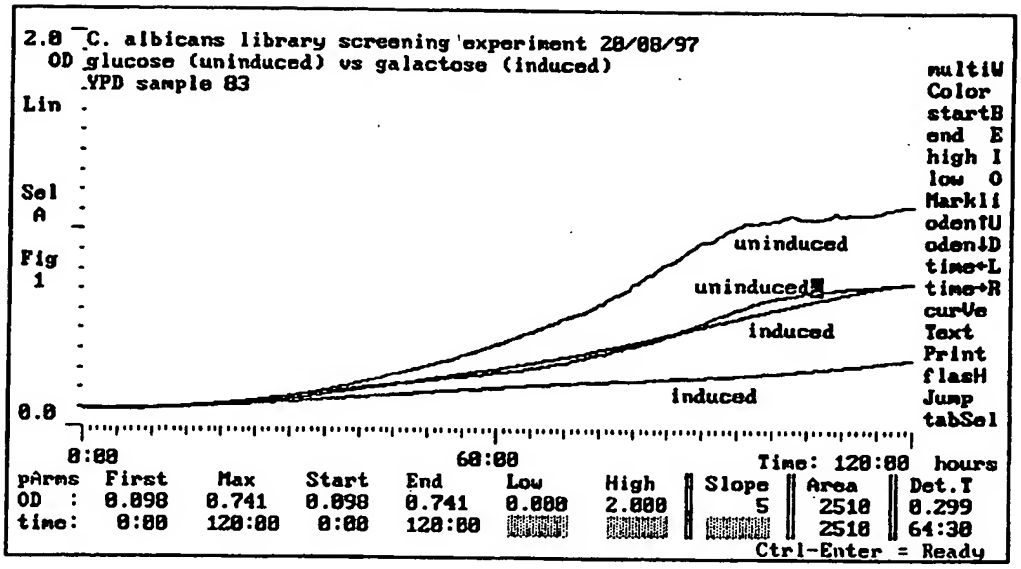


FIG. 63.



60/63

FIG. 64.



83c3 (SHA3)

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FIG. 65.

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 85g

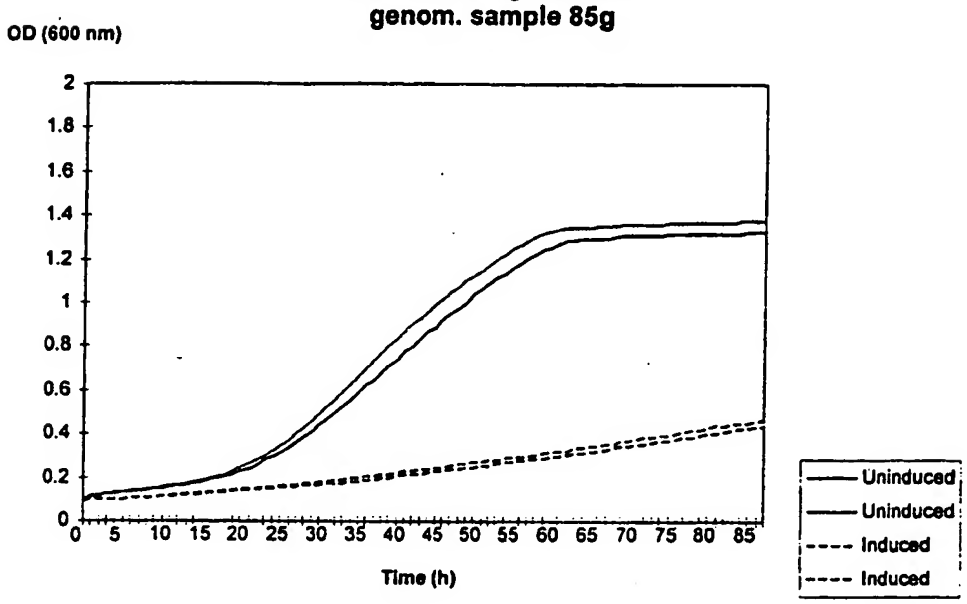


FIG. 66.

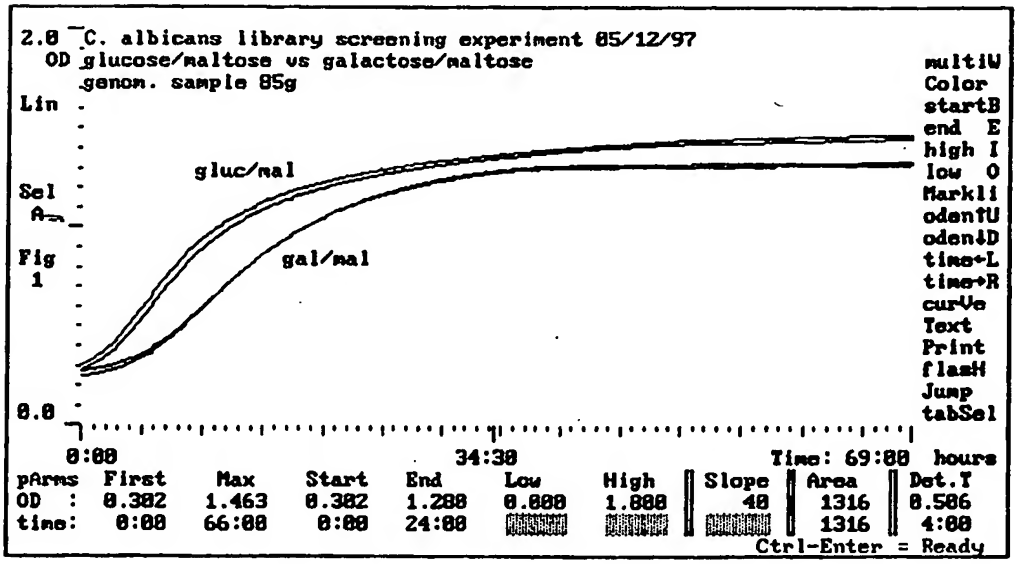


FIG. 67.

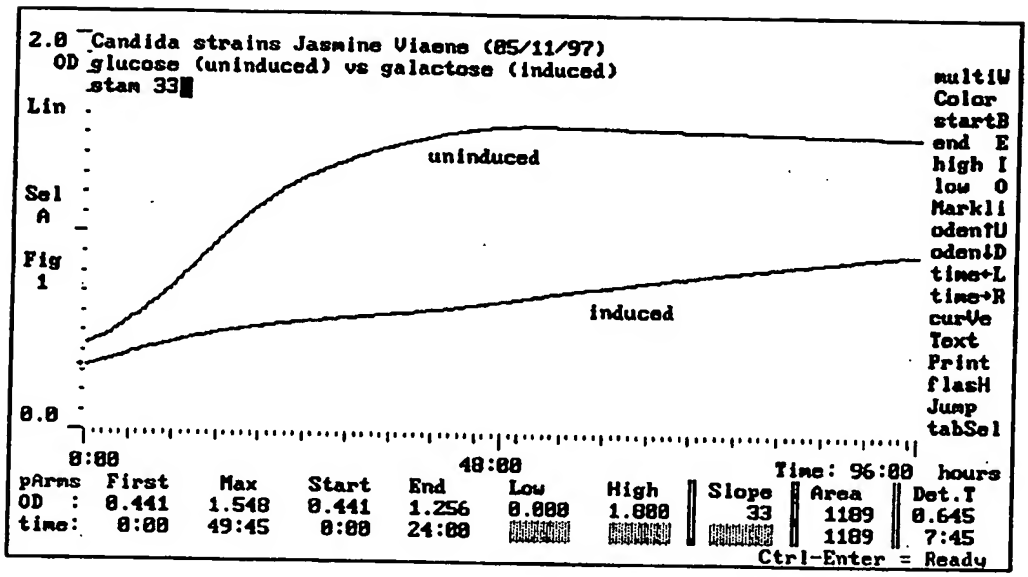

2.0
Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 33
Lin
Sel
A
Fig
1
uninduced
induced
0.0
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenfU
odenfD
timeL
timeR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.441 1.548 0.441 1.256 0.000 1.000 33 1189 0.645
time: 0:00 49:45 0:00 24:00 1189 7:45
Ctrl-Enter = Ready

FIG. 68.

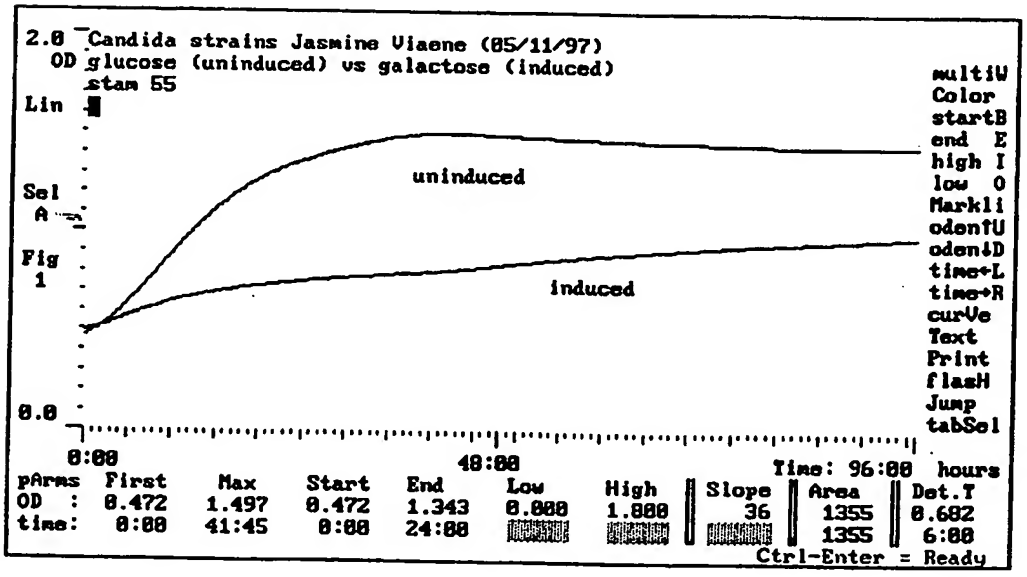

2.0
Candida strains Jasmine Vlaene (05/11/97)
OD glucose (uninduced) vs galactose (induced)
stam 55
Lin
Sel
A
Fig
1
uninduced
induced
0.0
0:00
48:00
Time: 96:00 hours
multiW
Color
startB
end E
high I
low O
Markli
odenfU
odenfD
timeL
timeR
curVe
Text
Print
flasH
Jump
tabSel
pArms First Max Start End Low High Slope Area Det.T
OD : 0.472 1.497 0.472 1.343 0.000 1.000 36 1355 0.682
time: 0:00 41:45 0:00 24:00 1355 6:00
Ctrl-Enter = Ready

FIG. 69.

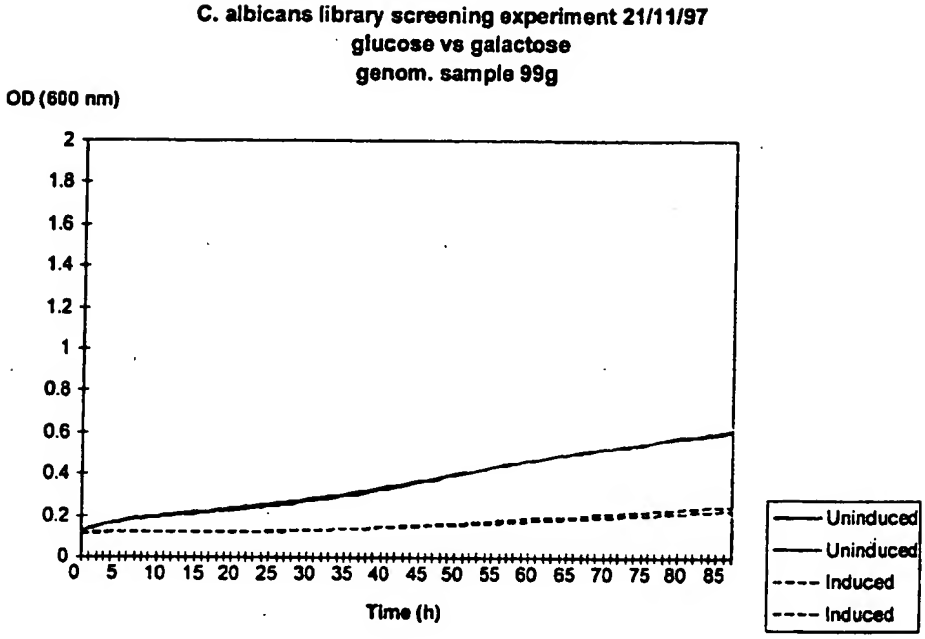
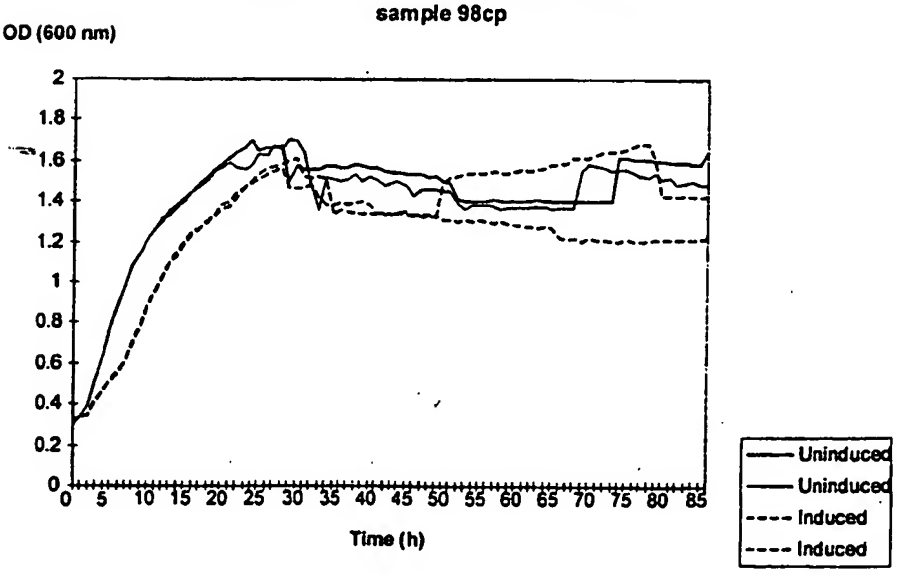

C. albicans library screening experiment 21/11/97
glucose vs galactose
genom. sample 99g
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85
Time (h)
Uninduced
Uninduced
Induced
Induced

FIG. 70.


C. albicans library screening experiment 24/04/98
glucose/maltose vs galactose/maltose
sample 98cp
OD (600 nm)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85
Time (h)
Uninduced
Uninduced
Induced
Induced

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International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

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98310694.9	23 December 1998 (23.12.98)	EP

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(72) Inventors; and

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(74) Agent: BOULT WADE TENNANT; 27 Furnival Street, London EC4A 1PQ (GB).

(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

With international search report.

Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(88) Date of publication of the international search report: 22 June 2000 (22.06.00)

(54) Title: DRUG TARGETS IN CANDIDA ALBICANS

(57) Abstract

The present invention is concerned with a method of identifying compounds which selectively modulate expression of polypeptides which are crucial for growth and survival of Candida albicans, which method comprises: (a) contacting a compound to be tested with one or more Candida albicans cells having a mutation in a nucleic acid molecule corresponding to the sequences according to any of claims 1 to 8 which mutation results in overexpression or underexpression of said polypeptides, in addition to contacting one or more wild type Candida albicans cells with said compound, (b) monitoring the growth and/or activity of said mutated cell compared to said wild type; wherein differential growth or activity of said one or more mutated Candida cells is indicative of selective action of said compound on a polypeptide or another polypeptide in the same or a parallel pathway. Also disclosed in the present invention are compounds identified and the sequences themselves which are critical for survival and growth of Candida albicans.

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ML	Mali
MN	Mongolia
MR	Mauritania
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MX	Mexico
NE	Niger
NL	Netherlands
NO	Norway
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SG	Singapore
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SK	Slovakia
SN	Senegal
SZ	Swaziland
TD	Chad
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INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 99/05991

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/31 C07K14/40 A61K31/70 A61K38/16 C07K16/14
G01N33/50 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K A61K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	REIFENBERGER E ET AL: "IDENTIFICATION OF NOVEL HXT GENES IN SACCHAROMYCES CEREVISIAE REVEALS THE IMPACT OF INDIVIDUAL HEXOSE TRANSPORTERS ON GLYCOLYTIC FLUX" MOLECULAR MICROBIOLOGY,GB,OXFORD, vol. 16, no. 1, 1 January 1995 (1995-01-01), pages 157-167, XP000572126	9,10,35
A	the whole document ---	23
A	EP 0 844 307 A (SMITHKLINE BEECHAM CORP) 27 May 1998 (1998-05-27) the whole document ---	24,38,39
	-/--	

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
1 February 2000	27.04.00

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Smart, R

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

Intern tal Application No
PCT/EP 99/05991

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DALY S ET AL: "Isolation and characterization of a gene encoding alpha-tubulin from Candida albicans" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES,GB,ELSEVIER SCIENCE PUBLISHERS, BARKING, vol. 187, no. 2, 7 April 1997 (1997-04-07), page 151-158 XP004093273 ISSN: 0378-1119 the whole document ---	
A	WO 97 36925 A (SCRIPTGEN PHARM INC ;HARVARD COLLEGE (US)) 9 October 1997 (1997-10-09) the whole document ---	
A	WO 97 37230 A (BRADLEY JOHN;WOBBE C RICHARD; BURATOWSKI STEPHEN) 9 October 1997 (1997-10-09) the whole document ---	
A	WO 96 36707 A (UNIV ROMA ;IST SUPERIORE SANITA (IT); CASSONE ANTONIO (IT); VALLE) 21 November 1996 (1996-11-21) the whole document -----	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 99/05991

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 25-28
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1,2,4-12,14-20,34,35,38,39 all partially

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 25-28

Claims 25-28 refer to a compound identifiable with a method, without giving a true technical characteization of the compound. Moreover, no such compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 83 and 84 EPC).
No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Invention 1: claims 1,2,4-12,14-28,34,35,38,39, all partially

Nucleic acid molecule comprising seq.ID.1 or capable of hybridizing thereto, polypeptide of seq.ID.43 encoded by said nucleic acid, expression vector comprising said nucleic acid, antibody against siad peptide, use of said vector for preparation of medicament or pharmaceutical composition, C. albicans cell comprising an induced mutation in said DNA sequence, oligonucleotides comprising 10-50 nt of said nucleic acid sequence, and method for identifying compounds which modulate expression of said nucleic acid.

2. Inventions 2-68: claims 1,6-11,15-28,34,35,38, 39 partially, and 2-5,12-14,36,37, 40 partially as applicable

As invention 1, but limited to the respective nucleic acid sequences 2,3,5,10,11,12,16,17,18,20,21,23,25,26,27,29,31, 33,35,37,39,41,44,45,46,49,50,52,55,57,59,61,63,65,67,70,72, 74,76,78,80,81,83,85,87,89,91,93,95,97,99,101,104,106,108,110 and 113, and polypeptide sequences corresponding to said nucleic acid sequences in as far as they are provided (see table 1 of the description), whereby invention 2 is limited to seq.ID.2, invention 3 is limited to seq.ID.3 and its translated polypeptide seq.ID.4, ..., and invention 68 is limited to seq.ID.113 and its translated polypeptide sequence seq.ID.114.

In as far as a polypeptide sequence, translated from the ORF of a corresponding nucleic acid sequence is provived, the polypeptide encoded by the corresponding nucleic acid sequence and their use in the preparation of a medicament, and antibodies against said polypeptide is also considered part of the respective invention.

3. Invention 69: claim 29-33

Method for identifying DNA sequences from a cell or organism, which encode polypeptides which are critical for growth and survival for said cell or organism, comprising screening a library of nucleic acids using a vector that either integrates into the genome of said cell or organism, or that permits expression of antisense RNA, and selecting growth-impaired cells or organisms. Plasmids pGAL1PSiST-1 and pGAL1PNiST-1, used in said method.

INTERNATIONAL SEARCH REPORT

Information on patent family members

Intern nal Application No
PCT/EP 99/05991

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SEQUENCE LISTING

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Val Phe Lys Lys Ala Arg Ser Thr Asn Ser Gly Ala Asp Glu Thr Gly
225                 230                 235                 240

Leu Met Ser Asp Lys Glu Phe Asp Asp Ser Ala Tyr Ser Pro Asp Tyr
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Leu Phe Glu Glu Asn Leu Trp Asn Lys Pro Asn His Pro Asp Thr Asn
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His Lys Thr Lys Lys Tyr Thr Glu Asn Val Val Glu Asn Leu Asp Ser
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<210> 12
<211> 1066
<212> DNA
<213> Candida albicans

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tgctattgga gcatatttgg caaatcacgt tttcaatgaa aaggaaaaat ttacaattga 780
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<210> 13
<211> 302
<212> PRT
<213> Candida albicans

<400> 13
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20 25 30

Glu Met Gln Lys Ile Ala Arg Trp Thr Asn Leu Ser Glu Thr Thr Phe

35 40 45

Ile Leu Thr Pro Lys Ser Ser Ile Ala Xaa Tyr Ser Ile Arg Ile Phe
50 55 60

Thr Ser Gly Gly Asn Glu Leu Pro Phe Ala Gly His Pro Thr Leu Gly
65 70 75 80

Thr Ala Phe Ala Leu Leu Glu Asp Gly Lys Ile Lys Pro Asn Asp Asn
85 90 95

Gly Gln Ile Ile Gln Glu Cys Gly Ala Gly Leu Val Lys Ile Ser Val
100 105 110

Glu Lys Thr Pro Asn Asn Asn Ser Asn Glu Leu Pro Phe Leu Leu Ser
115 120 125

Phe Glu Leu Pro Tyr Phe Lys Phe His Glu Ile Asp Asp Lys Val Ile
130 135 140

Glu Glu Leu Gln His Ser Trp Asn Gly Thr Asn Ile Ile Gly Lys Pro
145 150 155 160

Val Leu Ile Asp Ala Gly Pro Lys Trp Ala Val Phe Gln Leu Gly Ser
165 170 175

Gly Lys Glu Val Leu Asp Leu Asn Xaa Asp Leu Ala Gln Ile Glu Arg
180 185 190

Leu Ser Leu Glu Asn Gly Trp Thr Gly Ile Gly Val Phe Gly Lys His
195 200 205

Asn Glu Asn Gly Asp Ser Val Glu Leu Arg Asn Ile Ala Pro Ala Val
210 215 220

Gly Val Ala Glu Asp Pro Ala Cys Gly Ser Gly Ser Gly Ala Ile Gly
225 230 235 240

Ala Tyr Leu Ala Asn His Val Phe Asn Glu Lys Glu Lys Phe Thr Ile
245 250 255

Asp Ile Ser Gln Gly Lys Pro Ile Glu Arg Asp Ala Lys Ile Gln Val
260 265 270

Lys Val Asn Arg Leu Thr Thr Lys Asn Gly Asp Leu Ser Ile His Val
275 280 285

Gly Gly His Ala Ile Thr Cys Phe Glu Gly Thr Tyr Ser Ile

290 295 300

<210> 14
<211> 3726
<212> DNA
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cctaaa 3726

<210> 15
<211> 942
<212> PRT
<213> Candida albicans

<400> 15
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Ser Gly Ile Thr Lys Gln Pro Lys Ala Ser Lys Ile Phe Ser Pro Phe
20 25 30

Arg Val Leu Gly Asn Val Thr Asp Ser Thr Pro Phe Ala Met Gly Thr
35 40 45

Leu Gly Ser Thr Phe Tyr Ala Val Thr Ser Val Gly Arg Ser Phe Gln
50 55 60

Ile Tyr Asp Leu Ala Thr Leu His Leu Leu Phe Val Ser Gln Thr Gln
65 70 75 80

Thr Pro Ser Arg Ile Thr Ser Leu Ala Ala His His His Tyr Val Tyr
85 90 95

Ala Ser Tyr Gly Asp Arg Ile Gly Ile Phe Arg Arg Gly Arg Leu Glu
100 105 110

His Glu Leu Val Cys Glu Gly Asn Ser Thr Val Asn Gln Leu Leu Val
115 120 125

Phe Gly Glu Tyr Leu Ile Ala Thr Thr Leu Glu Gly Asp Ile Phe Val
130 135 140

Phe Arg Lys Thr Glu Gly Lys Lys Phe Pro Thr Glu Leu Tyr Thr Thr
145 150 155 160

Ile Arg Ile Ile Asn Ser Leu Val Glu Gly Glu Ile Val Gly Leu Ile
165 170 175

His Pro Pro Thr Tyr Leu Asn Lys Val Ile Val Ala Thr Thr Gln Ser
180 185 190

Val Phe Val Ile Asn Val Arg Thr Gly Lys Leu Leu Tyr Lys Ser Arg
195 200 205

Glu Leu Gln Phe Glu Gly Glu Lys Ile Ser Ser Ile Glu Ala Ala Pro
210 215 220

Val Leu Asp Val Ile Ala Val Gly Thr Ser Asn Gly Asn Val Phe Leu
225 230 235 240

Phe Asn Ile Lys Lys Gly Lys Val Leu Gly Gln Lys Ile Ile Thr Ser
245 250 255

Gly Thr Glu Ser Ser Ser Lys Val Ala Ser Ile Ser Phe Arg Thr Asp
260 265 270

Gly Ala Pro His Leu Val Ala Gly Leu Asn Asn Gly Asp Leu Tyr Phe
275 280 285

Tyr Asp Leu Asp Lys Lys Ser Arg Val His Val Leu Arg Asn Ala His
290 295 300

Lys Glu Thr His Gly Gly Val Ala Asn Ala Lys Phe Leu Asn Gly Gln
305 310 315 320

Pro Ile Val Leu Ser Asn Gly Gly Asp Asn His Leu Lys Glu Phe Val
325 330 335

Phe Asp Pro Asn Leu Thr Thr Ser Asn Ser Ser Ile Val Pro Pro Pro
340 345 350

Arg His Leu Arg Ser Arg Gly Gly His Ser Ala Pro Pro Val Ala Ile
355 360 365

Glu Phe Pro Gln Glu Asp Lys Thr His Phe Leu Leu Ser Ala Ser Arg
370 375 380

Asp Lys Thr Phe Trp Ile Phe Ser Leu Arg Lys Asp Ala Gln Ala Gln
385 390 395 400

Glu Met Ser Gln Arg Leu Gln Lys Ser Lys Asp Gly Lys Arg Gln Ala
405 410 415

Gly Gln Val Val Ser Met Arg Glu Lys Phe Pro Glu Ile Ile Ser Ile
420 425 430

Ser Ser Ser Tyr Ala Arg Glu Gly Asp Trp Glu Asn Ile Ile Thr Ala
435 440 445

His Lys Asp Glu Thr Phe Ala Arg Thr Trp Asp Ser Arg Asn Lys Arg
450 455 460

Val Gly Arg His Leu Leu Asn Thr Ile Asp Gly Gly Ile Val Lys Ser
465 470 475 480

Val Cys Val Ser Gln Cys Gly Asn Phe Gly Leu Val Gly Ser Ser Ser
485 490 495

Gly Gly Ile Gly Ser Tyr Asn Leu Gln Ser Gly Leu Leu Arg Lys Lys
500 505 510

Tyr Val Leu His Lys Gln Ala Val Thr Gly Leu Ala Ile Asp Gly Met
515 520 525

Asn Arg Lys Met Val Ser Cys Gly Leu Asp Gly Ile Val Gly Phe Tyr
530 535 540

Asp Phe Gly Lys Ser Val Tyr Leu Gly Lys Leu Gln Leu Glu Ala Pro
545 550 555 560

Ile Thr Ser Met Ile Tyr His Lys Ser Ser Asp Leu Val Ala Cys Ala
565 570 575

Leu Asp Asp Leu Ser Ile Val Val Ile Asp Val Thr Thr Gln Lys Val
580 585 590

Ile Arg Ile Leu Tyr Gly His Thr Asn Arg Ile Ser Gly Met Asp Phe
595 600 605

Ser Pro Asp Gly Arg Trp Ile Val Ser Val Ala Leu Asp Ser Thr Leu
610 615 620

Arg Thr Trp Asp Leu Pro Thr Gly Gly Cys Ile Asp Gly Val Ile Leu
625 630 635 640

Pro Ile Val Ala Thr Ala Val Lys Phe Ser Pro Ile Gly Asp Ile Leu
645 650 655

Ala Thr Thr His Val Ser Gly Asn Gly Val Ser Leu Trp Thr Asn Arg
660 665 670

Ala Gln Phe Lys Pro Val Ser Thr Arg His Val Glu Glu Asp Glu Phe
675 680 685

Ser Thr Ile Leu Leu Pro Asn Ala Ser Gly Asp Gly Gly Ser Thr Met
690 695 700

Leu Asp Gly Phe Leu Asp Glu Asp Ser Asn Glu Asp Gly Thr Ile Asp
705 710 715 720

Glu Gln Tyr Thr Ser Ala Ala Gln Ile Asp Ala Ser Leu Ile Thr Leu
725 730 735

Ser Ser Glu Pro Arg Ser Lys Phe Asn Thr Leu Leu His Leu Asp Thr
740 745 750

Ile Lys Gln Gln Ser Lys Pro Lys Glu Ala Pro Lys Lys Pro Glu Asn
755 760 765

Ala Pro Phe Phe Leu Gln Leu Thr Gly Gln Ala Val Gly Asp Arg Ala
770 775 780

Ser Val Ala Glu Gly Lys Thr Ser Glu Gln Thr Asn Asn Thr Val Glu
785 790 795 800

Glu Thr Asn Ser Lys Leu Arg Lys Leu Asp Thr Asn Gly Asn His Ala
805 810 815

Phe Glu Ser Glu Phe Thr Lys Leu Leu Arg Glu Ala Gly Glu Ser Gly
820 825 830

Gln Phe Glu Arg Phe Leu Thr Tyr Leu Leu Asn Leu Ser Pro Ala Val
835 840 845

Leu Asp Leu Glu Ile Arg Ser Leu Asn Ser Phe Val Pro Leu Thr Glu
850 855 860

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Met Thr Asn Phe Ile Gln Ala Leu Asn Ala Gly Leu Lys Ser Asn Ala
865                 870                 875                 880

Asn Tyr Glu Ile Trp Glu Thr Leu Tyr Ala Met Phe Phe Asn Ile His
                885                 890                 895

Gly Asp Val Ile His Gln Phe Glu Asn Glu Thr Ser Leu His Glu Ala
            900                 905                 910

Leu Glu Glu Tyr Arg Gln Leu Asn Asp Glu Lys Asn Asn Lys Met Asp
        915                 920                 925

Ser Leu Val Lys Tyr Cys Ala Ser Ile Val Ser Phe Ile Ser
    930                 935                 940
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<211> 725
<212> DNA
<213> Candida albicans

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agagagcaat gtaagtcttg atagtaatga gccgtgttga agtagtattt taatctaatt 180
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agaataagca gtaggaggtg tctgaattga gtttgtattg ttatttagag ttttaaatta 480
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aagtaattta gagtttaaac agggggcac gagtcagtgt tagagttgtg aagtttattt 660
ggctagtgaa ttgactggca agattgttaa acgtggggta gaaaaagaca acgcatcgac 720
aggtt 725

<210> 17
<211> 626
<212> DNA
<213> Candida albicans

<400> 17
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tggcgaaaaa aaaaaacaag atctactact ctgttggatt tatttgtgat ggcgattgaa 180
gagaaaacac gtctttttaa cgcgtttttt tatttttgg agaagcaaat ttcaagcaaa 240
gactcttatt gtgttgcttt tgatccattc aaattttgta ttacttttca ttagaactat 300

aactgttcat tatcaatgac gtatacatgt ctggttcctg ttatgtattg taattttagt 360
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cagcaacaag tgttattttc cctgaatgta gaaaatgaaa ggtagtgttt acatatagtt 480
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caattcaagt tgacgggtag ttttttttt ttcactgcat ttttcaacga aaactaaata 600
aaatttcgct gatattgata aagtat 626

<210> 18
<211> 667
<212> DNA
<213> Candida albicans

<400> 18
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atttagtgta caaatttctg ccaaaaaaat acaataaaaa ccgcttatag tcttctactg 180
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acagaac 667

<210> 19
<211> 5
<212> PRT
<213> Candida albicans

<400> 19
Met Pro Tyr Thr Glu
1 5

<210> 20
<211> 165
<212> DNA
<213> Candida albicans

<400> 20
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taaggtccca ttcaaattca ctaatgcaca attggatctt tatgctgcta gcacacataa 120
ccaagagcca atatcctagt aacgacgcac catagtagac cgaat 165

<210> 21
<211> 564

<212> DNA
<213> Candida albicans

<400> 21
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aaccatttaa tgccaactag atactcattg gatgttgaat cattcaaatc tgctgtcact 300
tctgaagctt tagaagaacc atctcaaaga gaagaagcta aaaaagttgt caagaaggct 360
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<210> 22
<211> 136
<212> PRT
<213> Candida albicans

<400> 22
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Arg Tyr Ala Gly Lys Lys Val Val Ile Val Lys Pro His Asp Glu Gly
20 25 30

Thr Lys Ser His Pro Phe Pro His Ala Ile Val Ala Gly Ile Glu Arg
35 40 45

Ala Pro Leu Lys Val Thr Lys Lys Met Asp Ala Lys Lys Val Thr Lys
50 55 60

Arg Thr Lys Val Lys Pro Phe Val Lys Leu Val Asn Tyr Asn His Leu
65 70 75 80

Met Pro Thr Arg Tyr Ser Leu Asp Val Glu Ser Phe Lys Ser Ala Val
85 90 95

Thr Ser Glu Ala Leu Glu Glu Pro Ser Gln Arg Glu Glu Ala Lys Lys
100 105 110

Val Val Lys Lys Ala Phe Glu Glu Lys His Gln Ala Gly Lys Asn Lys
115 120 125

Trp Phe Phe Gln Lys Leu His Phe
130 135

<210> 23
<211> 1192
<212> DNA
<213> Candida albicans

<400> 23
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<210> 24
<211> 336
<212> PRT
<213> Candida albicans

<400> 24
Met Ser Ile Pro Ser Thr Gln Tyr Gly Phe Phe Tyr Asn Lys Ala Ser
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Gly Leu Asn Leu Lys Lys Asp Leu Pro Val Asn Lys Pro Gly Ala Gly
20 25 30

Gln Leu Leu Leu Lys Val Asp Ala Val Gly Leu Cys His Ser Asp Leu
35 40 45

His Val Leu Tyr Glu Gly Leu Asp Cys Gly Asp Asn Tyr Val Met Gly
50 55 60

His Glu Ile Ala Gly Thr Val Ala Glu Leu Gly Glu Glu Val Ser Glu
65 70 75 80

Phe Ala Val Gly Asp Arg Val Ala Cys Val Gly Pro Asn Gly Cys Gly
85 90 95

Leu Cys Lys His Cys Leu Thr Gly Asn Asp Asn Val Cys Thr Lys Ser
100 105 110

Phe Leu Asp Trp Phe Gly Leu Gly Tyr Asn Gly Gly Tyr Glu Gln Phe
115 120 125

Leu Leu Val Lys Arg Pro Arg Asn Leu Val Lys Ile Pro Asp Asn Val
130 135 140

Thr Ser Glu Glu Ala Ala Ala Ile Thr Asp Ala Val Leu Thr Pro Tyr
145 150 155 160

His Ala Ile Lys Ser Ala Gly Val Gly Pro Ala Ser Asn Ile Leu Ile
165 170 175

Ile Gly Ala Gly Gly Leu Gly Gly Asn Ala Ile Gln Val Ala Lys Ala
180 185 190

Phe Gly Ala Lys Val Thr Val Leu Asp Lys Lys Asp Lys Ala Arg Asp
195 200 205

Gln Ala Lys Ala Phe Gly Ala Asp Gln Val Tyr Ser Glu Leu Pro Asp
210 215 220

Ser Val Leu Pro Gly Ser Phe Ser Ala Cys Phe Asp Phe Val Ser Val
225 230 235 240

Gln Ala Thr Tyr Asp Leu Cys Gln Lys Tyr Cys Glu Pro Lys Gly Thr
245 250 255

Ile Val Pro Val Gly Leu Gly Ala Thr Ser Leu Asn Ile Asn Leu Ala
260 265 270

Asp Leu Asp Leu Arg Glu Ile Thr Val Lys Gly Ser Phe Trp Gly Thr
275 280 285

Ser Met Asp Leu Arg Glu Ala Phe Glu Leu Ala Ala Gln Gly Lys Val
290 295 300

Lys Pro Asn Val Ala His Ala Pro Leu Ser Glu Leu Pro Lys Tyr Met
305 310 315 320

Glu Lys Leu Arg Ala Gly Gly Tyr Glu Gly Arg Val Val Phe Asn Pro
325 330 335

<210> 25
<211> 2481
<212> DNA
<213> Candida albicans

<400> 25
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<211> 826
<212> PRT
<213> Candida albicans

<400> 26
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Ser Ala Val Asp Asp Lys Thr Ala Thr Ala Ile Leu Arg Arg Lys Lys
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Lys Asp Asn Ala Leu Val Val Asp Asp Ala Thr Asn Asp Asp Asn Ser
35 40 45

Val Ile Thr Met Ser Ser Asn Thr Met Glu Leu Leu Gln Leu Phe Arg
50 55 60

Gly Asp Thr Val Leu Val Lys Gly Lys Lys Arg Lys Asp Thr Val Leu
65 70 75 80

Ile Val Leu Ala Asp Asp Asp Met Pro Asp Gly Val Ala Arg Val Asn
85 90 95

Arg Cys Val Arg Asn Asn Leu Arg Val Arg Leu Gly Asp Ile Val Thr
100 105 110

Val His Pro Cys Pro Asp Ile Lys Tyr Ala Asn Arg Ile Ser Val Leu
115 120 125

Pro Ile Ala Asp Thr Val Glu Gly Ile Asn Gly Ser Leu Phe Asp Leu
130 135 140

Tyr Leu Lys Pro Tyr Phe Val Glu Ala Tyr Arg Pro Val Arg Lys Gly
145 150 155 160

Asp Leu Phe Thr Val Arg Gly Gly Met Arg Gln Val Glu Phe Lys Val
165 170 175

Val Glu Val Asp Pro Glu Glu Ile Ala Ile Val Ala Gln Asp Thr Ile
180 185 190

Ile His Cys Glu Gly Glu Pro Ile Asn Arg Glu Asp Glu Glu Asn Ser
195 200 205

Leu Asn Glu Val Gly Tyr Asp Asp Ile Gly Gly Cys Lys Lys Gln Met
210 215 220

Ala Gln Ile Arg Glu Leu Val Glu Leu Pro Leu Arg His Pro Gln Leu
225 230 235 240

Phe Lys Ser Ile Gly Ile Lys Pro Pro Lys Gly Ile Leu Met Tyr Gly
245 250 255

Pro Pro Gly Thr Gly Lys Thr Ile Met Ala Arg Ala Val Ala Asn Glu
260 265 270

Thr Gly Ala Phe Phe Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys
275 280 285

Met Ala Gly Glu Ser Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala
290 295 300

Glu Lys Asn Ser Pro Ser Ile Ile Phe Ile Asp Glu Ile Asp Ser Ile
305 310 315 320

Ala Pro Lys Arg Asp Lys Thr Asn Gly Glu Val Glu Arg Arg Val Val
325 330 335

Ser Gln Leu Leu Thr Leu Met Asp Gly Met Lys Ala Arg Ser Asn Val
340 345 350

Val Val Ile Ala Ala Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu
355 360 365

Arg Arg Phe Gly Arg Phe Asp Arg Glu Val Asp Ile Gly Val Pro Asp
370 375 380

Ala Glu Gly Arg Leu Glu Ile Leu Arg Ile His Thr Lys Asn Met Lys
385 390 395 400

Leu Ala Asp Asp Val Asp Leu Glu Ala Ile Ala Ser Glu Thr His Gly
405 410 415

Phe Val Gly Ala Asp Ile Ala Ser Leu Cys Ser Glu Ala Ala Met Gln
420 425 430

Gln Ile Arg Glu Lys Met Asp Leu Ile Asp Leu Glu Glu Glu Thr Ile
435 440 445

Asp Thr Glu Val Leu Asn Ser Leu Gly Val Thr Gln Asp Asn Phe Arg
450 455 460

Phe Ala Leu Gly Asn Ser Asn Pro Ser Ala Leu Arg Glu Thr Val Val
465 470 475 480

Glu Asn Val Asn Val Thr Trp Asp Asp Ile Gly Gly Leu Asp Asn Ile
485 490 495

Lys Asn Glu Leu Lys Glu Thr Val Glu Tyr Pro Val Leu His Pro Asp
500 505 510

Gln Tyr Gln Lys Phe Gly Leu Ala Pro Thr Lys Gly Val Leu Phe Phe
515 520 525

Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Val Ala Thr
530 535 540

Glu Val Ser Ala Asn Phe Ile Ser Val Lys Gly Pro Glu Leu Leu Ser
545 550 555 560

Met Trp Tyr Gly Glu Ser Glu Ser Asn Ile Arg Asp Ile Phe Asp Lys
565 570 575

Ala Arg Ala Ala Ala Pro Thr Val Val Phe Leu Asp Glu Leu Asp Ser
580 585 590

Ile Ala Lys Ala Arg Gly Gly Ser His Gly Asp Ala Gly Gly Ala Ser
595 600 605

Asp Arg Val Val Asn Gln Leu Leu Thr Glu Met Asp Gly Met Asn Ala
610 615 620

Lys Lys Asn Val Phe Val Ile Gly Ala Thr Asn Arg Pro Asp Gln Ile
625 630 635 640

Asp Pro Ala Leu Leu Arg Pro Gly Arg Leu Asp Gln Leu Ile Tyr Val
645 650 655

Pro Leu Pro Asp Glu Pro Ala Arg Leu Ser Ile Leu Gln Ala Gln Leu
660 665 670

Arg Asn Thr Pro Leu Glu Pro Gly Leu Asp Leu Asn Glu Ile Ala Lys
675 680 685

Ile Thr His Gly Phe Ser Gly Ala Asp Leu Ser Tyr Ile Val Gln Arg
690 695 700

Ser Ala Lys Phe Ala Ile Lys Asp Ser Ile Glu Ala Gln Val Lys Ile
705 710 715 720

Asn Lys Ile Lys Glu Glu Lys Glu Lys Val Lys Thr Glu Asp Val Asp
725 730 735

Met Lys Val Asp Glu Val Glu Glu Glu Asp Pro Val Pro Tyr Ile Thr
740 745 750

Arg Ala His Phe Glu Glu Ala Met Lys Thr Ala Lys Arg Ser Val Ser
755 760 765

Asp Ala Glu Leu Arg Arg Tyr Glu Ser Tyr Ala Gln Gln Leu Gln Ala
770 775 780

Ser Arg Gly Gln Phe Ser Ser Phe Arg Phe Asn Glu Asn Ala Gly Ala
785 790 795 800

Thr Asp Asn Gly Ser Ala Ala Gly Ala Asn Ser Gly Ala Ala Phe Gly
805 810 815

Asn Val Glu Glu Glu Asp Asp Leu Tyr Ser
820 825

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<211> 1918
<212> DNA
<213> Candida albicans

<400> 27
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caaaaaatcc tcaccagaag aaaaaaaaat caatttcac aggtaaagtt gtacggacag 180
cacgacagac acaaaactaa agtaaatcca tgaggaaaaa agtaaaaaaa aaaaaattgt 240
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<210> 28
<211> 466
<212> PRT
<213> Candida albicans

<400> 28

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Thr Phe Lys Asn Ser Ile Arg Thr Tyr Ala Ser Ala Glu Pro Thr Leu
20 25 30

Lys Gln Arg Leu Glu Glu Ile Leu Pro Ala Lys Ala Glu Glu Val Lys
35 40 45

Gln Phe Lys Lys Glu His Gly Lys Thr Val Ile Gly Glu Val Leu Leu
50 55 60

Glu Gln Ala Tyr Gly Gly Met Arg Gly Ile Lys Gly Leu Val Trp Glu
65 70 75 80

Gly Ser Val Leu Asp Pro Ile Glu Gly Ile Arg Phe Arg Gly Arg Thr
85 90 95

Ile Pro Asp Ile Gln Lys Glu Leu Pro Lys Ala Pro Gly Gly Glu Glu
100 105 110

Pro Leu Pro Glu Ala Leu Phe Trp Leu Leu Leu Thr Gly Glu Val Pro
115 120 125

Thr Asp Ala Gln Thr Lys Ala Leu Ser Glu Glu Phe Ala Ala Arg Ser
130 135 140

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Ala Leu Pro Lys His Val Glu Glu Leu Ile Asp Arg Ser Pro Ser His
145                 150                 155                 160

Leu His Pro Met Ala Gln Phe Ser Ile Ala Val Thr Ala Leu Glu Ser
                165                 170                 175

Glu Ser Gln Phe Ala Gln Ala Tyr Ala Lys Gly Ala Asn Lys Ser Glu
            180                 185                 190

Tyr Trp Lys Tyr Thr Tyr Glu Asp Ser Ile Asp Leu Leu Ala Lys Leu
        195                 200                 205

Pro Thr Ile Ala Ala Lys Ile Tyr Arg Asn Val Phe His Asp Gly Lys
    210                 215                 220

Leu Pro Ala Ala Ile Asp Ser Lys Leu Asp Tyr Gly Ala Asn Leu Ala
225                 230                 235                 240

Ser Leu Leu Gly Phe Gly Asp Asn Lys Glu Phe Val Glu Leu Met Arg
                245                 250                 255

Leu Tyr Leu Thr Ile His Ser Asp His Glu Gly Gly Asn Val Ser Ala
            260                 265                 270

His Thr Thr His Leu Val Gly Ser Ala Leu Ser Ser Pro Phe Leu Ser
        275                 280                 285

Leu Ala Ala Gly Leu Asn Gly Leu Ala Gly Pro Leu His Gly Arg Ala
    290                 295                 300

Asn Gln Glu Val Leu Glu Trp Leu Phe Lys Leu Arg Glu Glu Leu Asn
305                 310                 315                 320

Gly Asp Tyr Ser Lys Glu Ala Ile Glu Lys Tyr Leu Trp Glu Thr Leu
                325                 330                 335

Asn Ser Gly Arg Val Val Pro Gly Tyr Gly His Ala Val Leu Arg Lys
            340                 345                 350

Thr Asp Pro Arg Tyr Thr Ala Gln Arg Glu Phe Ala Leu Lys His Met
        355                 360                 365

Pro Asp Tyr Glu Leu Phe Lys Leu Val Ser Asn Ile Tyr Glu Val Ala
    370                 375                 380

Pro Gly Val Leu Thr Lys His Gly Lys Thr Lys Asn Pro Trp Pro Asn
385                 390                 395                 400
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Val Asp Ser His Ser Gly Val Leu Leu Gln Tyr Tyr Gly Leu Thr Glu
405 410 415

Gln Ser Phe Tyr Thr Val Leu Phe Gly Val Ser Arg Ala Phe Gly Val
420 425 430

Leu Pro Gln Leu Ile Leu Asp Arg Gly Ile Gly Met Pro Ile Glu Arg
435 440 445

Pro Lys Ser Phe Ser Thr Glu Lys Tyr Ile Glu Leu Val Lys Asn Ile
450 455 460

Asn Lys
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<211> 2862
<212> DNA
<213> Candida albicans

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<210> 30
<211> 953
<212> PRT
<213> Candida albicans

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20 25 30

Ala Leu Leu Ser Gln Thr Asn Asn Asn Pro Thr Asn Asp Val Lys Phe
35 40 45

Ser Gln Ile Phe Leu Asp Leu Lys Lys Arg Ser Gln Asn Trp Lys Ser
50 55 60

Phe Asp Asp Ile Ile Gln Leu Ser Leu Leu Gln Leu Gln Tyr Cys Ile
65 70 75 80

Tyr Ala Lys Asn Ser Ile Lys Ala Lys Asp Arg Phe Asn Gly Ile Leu
85 90 95

Gln Thr Leu Leu Lys Lys Pro Gln Phe Asn Ile Ser Lys Ser Lys Asn
100 105 110

Leu Pro Ile Val Ser Lys Leu Gln Asn Phe Leu Ile Leu Gly Lys Phe
115 120 125

Gln Leu Leu Ala Cys His Val Asn Asn His Ile Ile His Asn Lys Ile
130 135 140

Glu Ala Phe Asn Asn Ile Lys Thr Gly Ile Gln Leu Leu Tyr Ser Ile
145 150 155 160

Val Lys Lys Leu Pro Thr Asn Ile Asn Lys Thr Leu Trp Gln Glu Leu
165 170 175

Asn Trp Glu Ile Thr Arg Leu Leu Phe Asp Ser Tyr Lys Leu Ala Ile
180 185 190

Asp Leu Ser Ile Asp Ile Gly Ile Ser Arg Asp Ile Pro Leu Phe Leu
195 200 205

Asn Glu Trp Val Lys Leu Asn Asn Ser Ile Asp Asn Asp Val Pro Ile
210 215 220

Val Asn Cys Ile Asn Glu Phe Glu Ile Gly Arg Tyr Gly Leu Leu Ser
225 230 235 240

Asn Asn Glu Phe Gln Lys Tyr Ile Arg Ile Ala Gln Gly Arg Leu Gly
245 250 255

Tyr Ser Leu Val Lys Asn Asn Ser Ala Val Gln Gln Tyr Ile Asn Arg
260 265 270

Asp Arg Asp Asp Glu Ile Cys Gly His Ala Ser Ser Ser Arg Gln Leu
275 280 285

Lys Ser Leu Val Arg Thr Ile Phe Asn Ser Asp Asn Ser Leu Ser Glu
290 295 300

Leu Ser Lys Ser Val Gln Leu Leu Pro Cys Ile Ile Gly Asp Ser Ser
305 310 315 320

Thr Met Cys Ser Lys Glu Leu Leu Asp Lys Leu Val Gln Leu Lys Asn
325 330 335

Glu Ile Leu Thr Glu Val Thr Asn Tyr Glu Lys Ser Ser Ser Leu Ser
340 345 350

Leu Asn Gln Gln Gln Gln Leu Ile Asn Asn Leu Asn Gln Val Val Cys
355 360 365

Leu Leu Ser Ser Leu Thr Ser Phe Lys Gly Asp Gly Leu Leu Ser Glu
370 375 380

Val Tyr Tyr Leu Gln Asp Tyr Val Arg Asn Leu Pro Phe Ala Asn Glu
385 390 395 400

Arg Lys Leu Met Asp Ser Ser Lys Gln Asp Glu Ser Asn Asn Leu Leu
405 410 415

Pro Arg Ala Leu Asp Phe Asn Gln Val Val Glu Asp Pro Ser Asn Thr
420 425 430

Thr Ile Asn Asn Ser Met Ile Asp Phe Asn Val Asp Leu Gln Leu Tyr
435 440 445

Leu Pro His Asn Trp Ile Leu Val Thr Leu Asp Ile Cys Gln Asn Thr
450 455 460

Gly Asp Leu Leu Ile Ser Lys Leu Thr Lys Gly Ser Pro Asn Pro Ile
465 470 475 480

Phe Met Arg Leu Pro Leu Ser Arg Phe Pro Ser Ser Leu Gly Phe Gln
485 490 495

Gln Leu Met Gln Asn Phe Glu Lys Ile Ile Asp Asp Ser Asn Leu Ser
500 505 510

Thr Lys Arg Lys Thr Thr Ser Lys Ile Leu Thr Val Glu Asp Arg Lys
515 520 525

Gln Trp Trp Arg Ser Arg Phe Thr Leu Asp Phe Gln Leu Gln Asp Ile
530 535 540

Leu His His Val Glu Ser Lys Trp Phe Gly Gly Phe Ile Ser Gly Ile
545 550 555 560

Phe Thr Asn Asp Asn Asp Val Glu Asn Glu Ser Lys Asn Val Phe His
565 570 575

Lys Phe Lys Gln Asp Leu Met Lys Ile Leu Lys Asp Cys Leu Thr Val
580 585 590

Ser Asp Asp Lys Ser Asn Ile Glu Arg Phe Leu Gln Phe Asn Glu Phe
595 600 605

Ile Tyr Tyr Cys Phe Tyr Ser Met Glu Glu Tyr Asn Tyr Glu Leu Val
610 615 620

Asp Asp Leu Ile Lys Phe Ile Thr Ile Asn Met Asn Ser His Gly Arg
625 630 635 640

Ile Val Asn Phe Gly Thr Asn Val Lys Ile Asn Lys Leu His Glu Leu
645 650 655

Ile Lys Asn Leu Ile Asp Lys Val Asn Lys Asn Lys Gln Asn Val Thr
660 665 670

Ser Asn Asn Lys Asn Asn Ser Asn Asn Asn Ser Asn Asn Asn Ser Asn
675 680 685

Ser Asn Asn Ser Gln His Ile Val Leu Ile Pro Asn Ala Asn Cys Ser
690 695 700

Asn Phe Pro Trp Glu Ser Met Glu Phe Leu Arg Ser Lys Ser Ile Ser
705 710 715 720

Arg Met Pro Ser Ile His Met Leu Leu Asp Leu Val Lys Ser Asn Thr
725 730 735

Asn Asn Lys Asn Lys Leu Met Phe Val Asp Lys Ser Asn Leu Tyr Tyr
740 745 750

Leu Ile Asn Pro Ser Gly Asp Leu Ile Arg Ser Glu Asn Arg Phe Lys
755 760 765

Lys Leu Phe Glu Ser Asn His Leu Trp Arg Gly Glu Ile Gly Lys Leu
770 775 780

Ser Ser Asn Glu His Glu Asp Tyr Gln Asp Ser Ile Leu Cys Glu Ile
785 790 795 800

Leu Lys Ser His Leu Phe Val Tyr Ile Gly His Gly Gly Cys Asp Gln
805 810 815

Tyr Ile Lys Val Ser Lys Leu Phe Lys Lys Cys Gly Asn Asn Gln Asp
820 825 830

Leu Ser Asn Lys Leu Pro Pro Ser Leu Leu Leu Gly Cys Ser Ser Val
835 840 845

Lys Leu Asp Asn Cys Asn Tyr Asn Tyr Asn Ser Ser Met Leu Gln Pro
850 855 860

Ser Gly Asn Ile Tyr Asn Trp Leu Asn Cys Lys Ser Ser Met Ile Leu
865 870 875 880

Gly Asn Leu Trp Asp Val Thr Asp Lys Asp Ile Asp Ile Phe Thr Leu
885 890 895

Ser Leu Leu Gln Lys Trp Gly Leu Ile Asp Asp Tyr Asn Gly Ser Gly
900 905 910

His Asp Tyr Gly Met Lys Lys Leu Asp Leu Thr Asn Cys Val Val Gln
915 920 925

Ser Arg Ser Lys Cys Thr Leu Lys Tyr Leu Asn Gly Ser Ala Pro Val
930 935 940

Val Tyr Gly Leu Pro Met Tyr Leu Lys
945 950

<210> 31
<211> 1443
<212> DNA
<213> Candida albicans

<400> 31
cttcttttag agacaatgca gtggttttct taccagatgc atgaccccca cccaataaaa 60
ctataatcga tctattcaca gtatttgatg ccattttgat ggtgatgaat gatgtgatgt 120
gatgctcatc ttattgggag tttcaaaaaa aaaagttaca ctcgaaaaaa aaaaaatagc 180
attataaata gaagctttac tatcttatag aacaaaacaa aaaacactat cttctaatta 240
ataatggatg attttgatag agatttagat aatgagttgg aatttagtca taaatcaacg 300
aaaggaataa aggttcatcg cacttttgaa agtatgaatt tgaaacctga tcttttgaaa 360
ggaatatatg cctatggatt tgaagcacca tctgctattc aatctagggc tattatgcag 420
atcatcagtg gtagagacac aatagcacag gcacaatctg gaactggtaa aactgctact 480
ttttctattg gtatgcttga ggttatagat actaaatcaa aagagtgtca agcacttatc 540
ttgtctccta ctagagagtt ggcaattcaa atacaaaatg tggtcatgca tttaggagat 600
tatatgaaca ttcacaccca tgcctgtatt ggtgggaaaa atgtcggtga ggatgttaag 660
aaattgcagc aagggcaaca aatagttagt gggacaccag gtagagtgat tgatgtgata 720
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ctttttacaa aagggtttaa agaacagatc tacgaaatct acaaacattt accaccttcg 840
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atatctacag atgtttgggc aagaggtatt gatgtccaac aagtctcgtt ggtaataaat 1260
tatgatttgc ccaccgataa ggaaaactat attcatagaa ttggacgatc aggtagattt 1320
ggtagaaagg gaacagctat aaacttgata actaaagatg atgtggtcac tttaaaagaa 1380

ttggagaaat attattcaac gaaaattaag gaaatgccaa tgaatattaa tgatataatg 1440
taa 1443

<210> 32
<211> 399
<212> PRT
<213> Candida albicans

<400> 32

Met Asp Asp Phe Asp Arg Asp Leu Asp Asn Glu Leu Glu Phe Ser His
1 5 10 15

Lys Ser Thr Lys Gly Ile Lys Val His Arg Thr Phe Glu Ser Met Asn
20 25 30

Leu Lys Pro Asp Leu Leu Lys Gly Ile Tyr Ala Tyr Gly Phe Glu Ala
35 40 45

Pro Ser Ala Ile Gln Ser Arg Ala Ile Met Gln Ile Ile Ser Gly Arg
50 55 60

Asp Thr Ile Ala Gln Ala Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe
65 70 75 80

Ser Ile Gly Met Leu Glu Val Ile Asp Thr Lys Ser Lys Glu Cys Gln
85 90 95

Ala Leu Ile Leu Ser Pro Thr Arg Glu Leu Ala Ile Gln Ile Gln Asn
100 105 110

Val Val Met His Leu Gly Asp Tyr Met Asn Ile His Thr His Ala Cys
115 120 125

Ile Gly Gly Lys Asn Val Gly Glu Asp Val Lys Lys Leu Gln Gln Gly
130 135 140

Gln Gln Ile Val Ser Gly Thr Pro Gly Arg Val Ile Asp Val Ile Lys
145 150 155 160

Arg Arg Asn Leu Gln Thr Arg Asn Ile Lys Val Leu Ile Leu Asp Glu
165 170 175

Ala Asp Glu Leu Phe Thr Lys Gly Phe Lys Glu Gln Ile Tyr Glu Ile
180 185 190

Tyr Lys His Leu Pro Pro Ser Val Gln Val Val Val Val Ser Ala Thr
195 200 205

Leu Pro Arg Glu Val Leu Glu Met Thr Ser Lys Phe Thr Thr Asp Pro
210 215 220

Val Lys Ile Leu Val Lys Arg Asp Glu Ile Ser Leu Ser Gly Ile Lys
225 230 235 240

Gln Tyr Tyr Val Gln Cys Glu Arg Glu Asp Trp Lys Phe Asp Thr Leu
245 250 255

Cys Asp Leu Tyr Asp Asn Leu Thr Ile Thr Gln Ala Val Ile Phe Cys
260 265 270

Asn Thr Lys Leu Lys Val Asn Trp Leu Ala Asp Gln Met Lys Lys Gln
275 280 285

Asn Phe Thr Val Val Ala Met His Gly Asp Met Lys Gln Asp Glu Arg
290 295 300

Asp Ser Ile Met Asn Asp Phe Arg Arg Gly Asn Ser Arg Val Leu Ile
305 310 315 320

Ser Thr Asp Val Trp Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu
325 330 335

Val Ile Asn Tyr Asp Leu Pro Thr Asp Lys Glu Asn Tyr Ile His Arg
340 345 350

Ile Gly Arg Ser Gly Arg Phe Gly Arg Lys Gly Thr Ala Ile Asn Leu
355 360 365

Ile Thr Lys Asp Asp Val Val Thr Leu Lys Glu Leu Glu Lys Tyr Tyr
370 375 380

Ser Thr Lys Ile Lys Glu Met Pro Met Asn Ile Asn Asp Ile Met
385 390 395

<210> 33
<211> 825
<212> DNA
<213> Candida albicans

<400> 33
aaccccacct tcaaagacaa agaagatttc gtcaagcaaa cgaatgtcag agcagaaaag 60
aaccaagaac taatcaaatt tgcccgtgac aaccttaacc atttaccatt caccgaaaaa 120
gacggaggtg catgggaaaa ctatgaacga atgatcagtg gtatgctcta caactgttta 180
caaaaagaat tggaaacaac acgtatgtct tgcagagact acatgttgga ctacggcagt 240
ttcagaacta gagattataa aacaacccaa gaatttcttg atgcaaaata caaacattta 300

gaaagtttca ttggacatgt tggcaaaaat gcatttatgg aatatccaat ctattttgat 360
tatgggttta acacttattt gggtgataat ttctattcca attacaattt gacaattttg 420
gatgtttcca tagtcagaat tggtaataat gtcaagtgtg gtcccaatgt atctatcctt 480
accccaacac acccagtgga tcccactttg cgctatgatc aattggaaaa tgccttgcct 540
gtgacggtgg gtaacggggt ctggttgtgt ggaagctgta ccattcttgg tggggtgaca 600
gtaggtgatg gcagcattgt ggctgctggt gcagttgtca acaaggacgt tccaccaaac 660
actgtagttg cgggagttcc tgctagggta gttaagcagc tagaacctag agaccctaac 720
tttgacacta tggcagtttt gaaacaatat ggtatgggtt atatagatta gtaattagat 780
ttgatgtaat gtacacgact acactatttg ctggtgtctg ttttt 825

<210> 34
<211> 206
<212> PRT
<213> Candida albicans

<400> 34
Met Ile Ser Gly Met Leu Tyr Asn Cys Leu Gln Lys Glu Leu Glu Thr
1 5 10 15

Thr Arg Met Ser Cys Arg Asp Tyr Met Leu Asp Tyr Gly Ser Phe Arg
20 25 30

Thr Arg Asp Tyr Lys Thr Thr Gln Glu Phe Leu Asp Ala Lys Tyr Lys
35 40 45

His Leu Glu Ser Phe Ile Gly His Val Gly Lys Asn Ala Phe Met Glu
50 55 60

Tyr Pro Ile Tyr Phe Asp Tyr Gly Phe Asn Thr Tyr Leu Gly Asp Asn
65 70 75 80

Phe Tyr Ser Asn Tyr Asn Leu Thr Ile Leu Asp Val Ser Ile Val Arg
85 90 95

Ile Gly Asn Asn Val Lys Cys Gly Pro Asn Val Ser Ile Leu Thr Pro
100 105 110

Thr His Pro Val Asp Pro Thr Leu Arg Tyr Asp Gln Leu Glu Asn Ala
115 120 125

Leu Pro Val Thr Val Gly Asn Gly Val Trp Leu Cys Gly Ser Cys Thr
130 135 140

Ile Leu Gly Gly Val Thr Val Gly Asp Gly Ser Ile Val Ala Ala Gly
145 150 155 160

Ala Val Val Asn Lys Asp Val Pro Pro Asn Thr Val Val Ala Gly Val
165 170 175

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Pro Ala Arg Val Val Lys Gln Leu Glu Pro Arg Asp Pro Asn Phe Asp
            180                 185                 190

Thr Met Ala Val Leu Lys Gln Tyr Gly Met Gly Tyr Ile Asp
        195                 200                 205
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20 25 30

Gln Ile Ser Ile Ala Lys Val Asp Glu Asp Gly Arg Ala Ile Ala Gly
35 40 45

Glu Asn Ile Thr Tyr Ala Leu Ser Gly Tyr Val Arg Gly Arg Gly Glu
50 55 60

Ala Asp Asp Ser Leu Asn Arg Leu Ala Gln Gln Asp Gly Leu Leu Lys
65 70 75 80

Asn Val Trp Ser Tyr Ser Arg
85

<210> 39
<211> 1685
<212> DNA
<213> Candida albicans

<400> 39
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tggtacctat ggtttgattt accttgtgga aaatatctac actaaacaac aatttgctgc 120
taaaatggtt cttgaacagc cattactcaa acaaaagcaa caacaacaac aaagtcatca 180
tggacataaa ggagaatcta gtatgaacaa acaaataata ctgcaagaat tttatcaata 240
ttttttaaac aatagtatgc cacaaccacg aaatttggac ttgaattacc ttcgagacaa 300
cggacatgat tgccccttttt tgactgaaat ctcattacat ttaaaagtac atcaacaccc 360
aaacatagcg actattcatc aagtattaaa cattgaagat tttgccataa taatattgat 420
ggatcatttt gagcaaggag atttgttcac taatatcatt gatagacaaa tattcaccaa 480
taatagtcat agaaaagttc caagaacaga ttttgaaacc caattattaa tgaagaatgc 540
catgttacaa ttgatagaag ccattgaata ttgtcacgaa aataatattt accattgtga 600
tttaaaacca gaaaacatta tggttagata taatccatac tatgttcgtc caactatcaa 660
taacaataat aacaatggag aagatgattt atgctatgcc aacagtatta ttgactataa 720
tgaattacac ctcgtgttga ttgattttgg tttagctatg gactctgcta ccatttgttg 780
taattcatgt cgtggatcgt cattttacat ggcaccagaa agaaccacca attataacac 840
ccatcgttta atcaaccaat taattgatat gaatcaatat gagtcaattg aaatcaatgg 900
gacaacagtg acaaaatcaa actgtaaata tttacctaca ttggctgggg atatttggtc 960
attgggagta ttgttcatta atatcacttg ttcaagaaac ccatggccca ttgcatcatt 1020
tgataataat caaaataatg aagtgtttaa gaattatatg ttgaataata acaaggctgt 1080
tttgagcaaa atcttaccca tttcctcaca atttaatcgc ttattagata gaattttcaa 1140
attgaatcct aatgatagaa tagatttacc aactttatac aaagaagtta ttcgttgtga 1200
tttcttcaaa gatgatcatt actactatgc ccaacatcaa catcatcaca atcacaatca 1260
aatcaataat gcttacaatc actatcagaa acaacctaat caagcaagac ctactgcaaa 1320
ccaacaattg tatacaccac cggaaaccac cacttataat tcatacgcta gtgatatgga 1380
agaagatgaa attagtgatg atgagtttta ttctgatgaa gaagatgaag atattgaaga 1440
ctatgaagag gaagaggaag agtattttgg taatgagcaa caacaacaac agcaagtcac 1500
aacagtgaat ggtaattttg gtcaagttaa aggtacctgt tattacgata ccaaaaccaa 1560
aacaactaca tatataaaac caccagctgc atatacttta gagacgccta gtcaaagtgt 1620

tgaatactgt taagttgtac acataaataa ttaatgacaa ttaataataa cgattaataa 1680
tatag 1685

<210> 40
<211> 537
<212> PRT

Ser Asp Glu Glu Asp Glu Asp Ile Glu Asp Tyr Glu Glu Glu Glu Glu
465 470 475 480

Glu Tyr Phe Gly Asn Glu Gln Gln Gln Gln Gln Val Thr Thr Val
485 490 495

Asn Gly Asn Phe Gly Gln Val Lys Gly Thr Cys Tyr Tyr Asp Thr Lys
500 505 510

Thr Lys Thr Thr Thr Tyr Ile Lys Pro Pro Ala Ala Tyr Thr Leu Glu
515 520 525

Thr Pro Ser Gln Ser Val Glu Tyr Cys
530 535

<210> 41
<211> 848
<212> DNA
<213> Candida albicans

<400> 41
aaccaatttt agaaacaatg gctcgtcaat ttttcgtagg tggtaacttc aaagctaacg 60
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atgtcgaagt tgtcatttgt ccacccgccc tttaccttgg tttagctgta gagcaaaaca 180
aacaaccaac tgttgccatt ggtgctcaaa atgtttttga caagtcatgt ggtgctttca 240
ctggtgaaac ctgtgcttct caaatcttgg atgttggtgc cagctggact ttaactggtc 300
acagtgaaag aagaaccatt atcaaagaat ccgatgaatt cattgctgaa aaaaccaagt 360
ttgccttgga cactggtgtc aaagttattt tatgtattgg tgaaacctta gaggaaagaa 420
aaggtggtgt cactttggat gtttgtgcca gacaattgga tgctgtttcc aagattgttt 480
ctgattggtc aaacattgtt gttgcttacg aacctgtttg ggcaattggt actggtttag 540
ccgctacccc agaagatgct gaagaaaccc acaaaggtat tagagctcat ttggccaaga 600
ccattggtgc cgaacaagct gaaaaaacca gaatcttgta cggtggttca gttaacggta 660
agaacgctaa ggatttcaaa gacaaagcaa atgttgatgg tttcttagtc ggtggtgctt 720
cattaaaacc agaatttgtt gatatcatca aatctagatt ataaacagta tattaaaaac 780
gatatgccta tagaatttag catgttgttg tgaatttgta atgaatctat aaaaatgtgc 840
tcatgaac 848

<210> 42
<211> 248
<212> PRT
<213> Candida albicans

<400> 42
Met Ala Arg Gln Phe Phe Val Gly Gly Asn Phe Lys Ala Asn Gly Thr
1 5 10 15

Lys Gln Gln Ile Thr Ser Ile Ile Asp Asn Leu Asn Lys Ala Asp Leu

```
            20                  25                  30

Pro Lys Asp Val Glu Val Val Ile Cys Pro Pro Ala Leu Tyr Leu Gly
        35                  40                  45

Leu Ala Val Glu Gln Asn Lys Gln Pro Thr Val Ala Ile Gly Ala Gln
    50                  55                  60

Asn Val Phe Asp Lys Ser Cys Gly Ala Phe Thr Gly Glu Thr Cys Ala
65                  70                  75                  80

Ser Gln Ile Leu Asp Val Gly Ala Ser Trp Thr Leu Thr Gly His Ser
                85                  90                  95

Glu Arg Arg Thr Ile Ile Lys Glu Ser Asp Glu Phe Ile Ala Glu Lys
            100                 105                 110

Thr Lys Phe Ala Leu Asp Thr Gly Val Lys Val Ile Leu Cys Ile Gly
        115                 120                 125

Glu Thr Leu Glu Glu Arg Lys Gly Gly Val Thr Leu Asp Val Cys Ala
    130                 135                 140

Arg Gln Leu Asp Ala Val Ser Lys Ile Val Ser Asp Trp Ser Asn Ile
145                 150                 155                 160

Val Val Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Leu Ala Ala
                165                 170                 175

Thr Pro Glu Asp Ala Glu Glu Thr His Lys Gly Ile Arg Ala His Leu
            180                 185                 190

Ala Lys Thr Ile Gly Ala Glu Gln Ala Glu Lys Thr Arg Ile Leu Tyr
        195                 200                 205

Gly Gly Ser Val Asn Gly Lys Asn Ala Lys Asp Phe Lys Asp Lys Ala
    210                 215                 220

Asn Val Asp Gly Phe Leu Val Gly Gly Ala Ser Leu Lys Pro Glu Phe
225                 230                 235                 240

Val Asp Ile Ile Lys Ser Arg Leu
                245
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<210> 43
<211> 550
<212> PRT

<213> Candida albicans

<400> 43

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Met Ser Leu Asp Asn Ser Thr Glu Asn Arg Asp Leu Glu Glu Lys Glu
 1               5                  10                  15

Glu Ile Pro Lys Asn Glu His Asn Glu Gln Gly Glu Gln Asn Glu Asn
            20                  25                  30

Asn Glu His Ile Pro Thr Leu Glu Asp Lys Pro Leu Lys Glu Tyr Ile
        35                  40                  45

Gly Ile Ser Ile Leu Cys Phe Leu Ile Ala Phe Gly Gly Phe Val Phe
    50                  55                  60

Gly Phe Asp Thr Gly Thr Ile Ser Gly Phe Ile Asn Met Thr Asp Phe
65                  70                  75                  80

Leu Glu Arg Phe Gly Gly Thr Lys Ala Asp Gly Thr Leu Tyr Phe Ser
                85                  90                  95

Asn Val Arg Thr Gly Leu Leu Ile Gly Leu Phe Asn Val Gly Cys Ala
            100                 105                 110

Ile Gly Ala Leu Phe Leu Ser Lys Val Gly Asp Met Tyr Gly Arg Arg
        115                 120                 125

Val Gly Ile Met Thr Ala Met Ile Ile Tyr Ile Val Gly Ile Ile Val
    130                 135                 140

Gln Ile Ala Ser Gln His Ala Trp Tyr Gln Ile Met Ile Gly Arg Ile
145                 150                 155                 160

Ile Thr Gly Leu Ala Val Gly Met Leu Ser Val Leu Cys Pro Leu Phe
                165                 170                 175

Ile Ser Glu Val Ser Pro Lys His Leu Arg Gly Thr Leu Val Tyr Cys
            180                 185                 190

Phe Gln Leu Met Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Ser
        195                 200                 205

Tyr Gly Thr Lys Lys Tyr Ser Asp Ser Arg Gln Trp Arg Ile Pro Leu
    210                 215                 220

Gly Leu Cys Phe Ala Trp Ala Leu Cys Leu Leu Gly Gly Met Val Arg
225                 230                 235                 240
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Met Pro Glu Ser Pro Arg Tyr Leu Val Gly Lys Asp Arg Ile Asp Asp
245 250 255

Ala Lys Ile Ser Leu Ala Lys Thr Asn Lys Val Ser Pro Glu Asp Pro
260 265 270

Ala Leu Tyr Arg Glu Leu Gln Leu Ile Gln Ala Gly Val Glu Arg Glu
275 280 285

Arg Leu Ala Gly Lys Ala Ser Trp Gly Ala Leu Ile Thr Gly Lys Pro
290 295 300

Arg Ile Leu Glu Arg Val Ile Val Gly Gly Met Leu Gln Ser Leu Gln
305 310 315 320

Gln Leu Thr Gly Asp Asn Tyr Phe Phe Tyr Tyr Ser Thr Thr Ile Phe
325 330 335

Lys Ser Val Gly Leu Asn Asp Ser Phe Glu Thr Ser Ile Ile Leu Gly
340 345 350

Val Ile Asn Phe Ala Ser Thr Phe Val Gly Ile Tyr Ala Ile Glu Arg
355 360 365

Leu Gly Arg Arg Leu Cys Leu Leu Thr Gly Ser Val Ala Met Ser Ile
370 375 380

Cys Phe Leu Ile Tyr Ser Leu Ile Gly Thr Gln His Leu Tyr Ile Asp
385 390 395 400

Gln Pro Gly Gly Pro Thr Arg Lys Pro Asp Gly Asn Ala Met Ile Phe
405 410 415

Ile Thr Ala Leu Tyr Val Phe Phe Phe Ala Ser Thr Trp Ala Gly Gly
420 425 430

Val Tyr Ser Ile Val Ser Glu Leu Tyr Pro Leu Lys Val Arg Ser Lys
435 440 445

Ala Met Gly Phe Ala Asn Ala Cys Asn Trp Leu Trp Gly Phe Leu Ile
450 455 460

Ser Phe Phe Thr Ser Phe Ile Thr Asp Ala Ile His Phe Tyr Tyr Gly
465 470 475 480

Phe Val Phe Met Gly Cys Leu Val Phe Ser Ile Phe Phe Val Tyr Phe
485 490 495

Met Ile Tyr Glu Thr Lys Gly Leu Thr Leu Glu Glu Ile Asp Glu Leu
500 505 510

Tyr Ser Thr Lys Val Val Pro Trp Lys Ser Ala Gly Trp Val Pro Pro
515 520 525

Ser Asp Glu Glu Met Val Arg Ala Lys Gly Tyr Thr Gly Asp Ile His
530 535 540

Ala Asp Glu Glu Gln Val
545 550

<210> 44
<211> 508
<212> DNA
<213> Candida albicans

<400> 44
ttcatgatta tatgatttca tttaatatat tgatttaata tatatattta attactcata 60
tagtcgtatt acacctgtag cccaattcat aagggtcatg cggattagtc ttcagcctct 120
acttcccata atatatctat tatgcatcac taattatagt aggcccgacc ataggtcggg 180
cttacttaaa tagtcgaggg ttgcgttcat tatataacta aataaaatac cacttggcat 240
gaactgacga caacaatgta acgcctgtat atactcgttc aggtaatgag tatatattca 300
agaattggta aggtgttagg ggtatcatcc aattaaacag cataatccac tgtacctgta 360
tataaccgtc taatgtattg catttcatcc gtgaggacgt actagtctgg cggtgtactt 420
caagtattaa cgtacccata atgaaagtta taggtttata aacccataac tatcttacat 480
atacgtagta cacatagttt acggctac 508

<210> 45
<211> 863
<212> DNA
<213> Candida albicans

<400> 45
ctcgtgcata attatcttaa aaccgtagat aagcaaaaat ttatcttatg aaatgttcag 60
cgataaagaa agaaagaatc aggtaccacg aggagtgttt ttgagaaaaa caactcgtaa 120
attaatgaat ctagtttctc tatacttgaa taatttttga gttttctgga aaagacacct 180
gttccagttt caaattaaac aagaatgtga aaagaataaa atttgattta ttctagcctg 240
ttaataatcc aggaaaactc aattttcgta attggcaact tgtccgagtg gttaaggaga 300
aagattagaa atcttttggg ctttgcccgc gcaggttcga gtcctgcagt tgtcgttatt 360
ttttttggtt tactctctat tttaaaattt aaaactaatc aactgaaact ggagtacctg 420
ccatgatatg agtaaatact tttttgatat taaaaatcta tataaaactc cctatttatt 480
ttttaattta aacccagata ttgtcccaat aatagttttt tgtttgaact tattgctttg 540
tatgaacctt gttagtttaa tctttccaat ttcatactct cttagttggc cacatcagtg 600
gctcattgaa taattctgat cttgaagtgt accagatgta ttctgacaaa actgcacacg 660
gacccagtca atagcattat agatattttg atttaaagtt caccgaatat atcgaatatc 720
tttattggcc atctcatctc atcttcttgc aataaattct taaacgctac tttttctcaa 780

accttattat ccctctagat actcttccaa atcttcaggt tcaaatatca ctttaaccat 840
caatgaacaa ctagggcaaa cag 863

<210> 46
<211> 925
<212> DNA
<213> Candida albicans

<400> 46
atgggtgcta cttgcccttt acggaaagtg gctacacacc gcaatgggtt accgatttgg 60
gaagctagta gggctaccag agctaccaaa gtattgtggg agagttgggt acagtacaca 120
ttgttacgca atgagttacc aattcgggaa gctagtaggg ctaccagagc taggttccag 180
ttaccaattc gggaagctag tagagctacc agagctgggt tccagttacc gatttaggaa 240
gtgtgttgca agcagggcta ccaaatatgg gtggcaacac atatggtaat aagtgctacc 300
aatgtgggtg caaaaaattt tgccaagtaa tttgtatggc aataacagaa gtgttggcgg 360
attcgaactc aggaatcttt ggtgtgtaaa aaaaaagcaa tagcgactac gctacaagag 420
gcaatcgatt attattataa agtggaagtt atatatatgt tgtcgggggg gggtaggggc 480
gctgcgcgcc cctgactttg acgggcccga cgcgggtttg ggttgtgatg gggcggtaaa 540
taataaggat tctccctccc ttttttctct ttcccccccc cctcctcccc ctttcccctt 600
ttccccgagt ctacaaatct acaagaggcc cgacggtgga ggcctgaggc cgaaggtcga 660
aggccgacaa agatgggtgg gtgggtggga ggttgtgttc ggggcgtagc cccgagaaaa 720
ttttggaata cagggccagg agggtagggg aaatggggaa aatgggggat ttgggaggga 780
atggggaagg aagaagaaga aaaaagtggt ggaaaggaga agatttttt tgggagaaaa 840
aatttttttt ataccaccga gaagtgtgag aggatacgat gggtgcgaca gggggtagag 900
ctgttgacaa cgttatatgg gggag 925

<210> 47
<211> 78
<212> PRT
<213> Candida albicans

<400> 47
Met Gly Ala Thr Cys Pro Leu Arg Lys Val Ala Thr His Arg Asn Gly
1 5 10 15

Leu Pro Ile Trp Glu Ala Ser Arg Ala Thr Arg Ala Thr Lys Val Leu
20 25 30

Trp Glu Ser Trp Val Gln Tyr Thr Leu Leu Arg Asn Glu Leu Pro Ile
35 40 45

Arg Glu Ala Ser Arg Ala Thr Arg Ala Arg Phe Gln Leu Pro Ile Arg
50 55 60

Glu Ala Ser Arg Ala Thr Arg Ala Gly Phe Gln Leu Pro Ile
65 70 75

<210> 48
<211> 81
<212> PRT
<213> Candida albicans

<400> 48
Met Gly Tyr Arg Phe Gly Lys Leu Val Gly Leu Pro Glu Leu Pro Lys
1 5 10 15

Tyr Cys Gly Arg Val Gly Tyr Ser Thr His Cys Tyr Ala Met Ser Tyr
20 25 30

Gln Phe Gly Lys Leu Val Gly Leu Pro Glu Leu Gly Ser Ser Tyr Gln
35 40 45

Phe Gly Lys Leu Val Glu Leu Pro Glu Ser Gly Ser Ser Tyr Arg Phe
50 55 60

Arg Lys Cys Val Ala Ser Arg Ala Thr Lys Tyr Gly Trp Gln His Ile
65 70 75 80

Trp

<210> 49
<211> 759
<212> DNA
<213> Candida albicans

<400> 49
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tggttgtgct gtataggagg ggtaagaatt tgccattctg ccccttttggg tgggtcagtc 180
aaaaaaagag gtatcactct ggttcaaacg ggaaacaaca gaaaatggga taaaaataat 240
ctccagacca aacttagtag taacagccat tttagttgta ctggtatacc ctacacaagt 300
tgtccatttt gtatggggaa ggggaattta gacaaaattt ttttttttgaa tttcgctaag 360
tgtcaagacc cgcaaaagtc acctttttttc gttttcaact atggcagagg ctcacctttt 420
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cgagtgggga gagtctggaa gtgatataca catcacgacc tactttatac gctacgttcg 660
gcatgggcga gccactgtac ggtggcaagc ctgaacagtc ccacaccaga tatctaacga 720
ttctgtgtat gggcactgat ggatttagtg gattactag 759

<210> 50
<211> 902
<212> DNA

<213> Candida albicans

<400> 50
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gtgacagctc tcaacatggc caactctgct gacgatctag caaaagtttt caaagattcg 180
actaaaaaat atcaaatcaa accaattatc aaatcagaca gtgatgaaca aatgattatc 240
aacattccat ttcttaatgg tagtgtcaaa ttgtattcga taattctacg taccaatggg 300
gatttgtatt gtcccaaaac aataaaatta ttcaaaaatg acacatcaat tgattttgat 360
aatgtggatt cgaagaaacc aatacaggtg ttaactcatc ctcaagttgg tgttgctaat 420
aatgatagcg atgatcttcc agagtttttg gaatcaaata acgatgacga ttttgtcgaa 480
cattatgtgt ctcgacataa attcactggg gtaaatcaat tgacaatatt tattgaagat 540
atttatgatg aaggagaaga agagtgtcat ttacattcaa ttgaattgag aggggaattc 600
actgaattaa acaaagaccc tgtcattaca ttatatgaac tggctgctaa tcctgctgat 660
cataagaatt taacgattgt tgaaaatcaa aatctagcat aaaacaaaga agtgaaaggt 720
atcagataag ctggttacat tacaattgat ctaatttaga atctcaaggt atttaaattt 780
gccgttttgc gataatataa catggtcaag aacgttgaat cgattacgtt aatggtttag 840
ctaattgatt tttaggatcg agtatttaga gtgaataaac aataaacaag aatgatgaat 900
tg 902

<210> 51
<211> 233
<212> PRT
<213> Candida albicans

<400> 51
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Asn His Asn His Val Ala Pro Ile Pro Thr Thr Ala Gly Gln Ser Leu
20 25 30

Asn Asn Lys Ile Asp Thr Ser Lys Val Thr Ala Leu Asn Met Ala Asn
35 40 45

Ser Ala Asp Asp Leu Ala Lys Val Phe Lys Asp Ser Thr Lys Lys Tyr
50 55 60

Gln Ile Lys Pro Ile Ile Lys Ser Asp Ser Asp Glu Gln Met Ile Ile
65 70 75 80

Asn Ile Pro Phe Leu Asn Gly Ser Val Lys Leu Tyr Ser Ile Ile Leu
85 90 95

Arg Thr Asn Gly Asp Leu Tyr Cys Pro Lys Thr Ile Lys Leu Phe Lys
100 105 110

Asn Asp Thr Ser Ile Asp Phe Asp Asn Val Asp Ser Lys Lys Pro Ile

115 120 125

Gln Val Leu Thr His Pro Gln Val Gly Val Ala Asn Asn Asp Ser Asp
130 135 140

Asp Leu Pro Glu Phe Leu Glu Ser Asn Asn Asp Asp Asp Phe Val Glu
145 150 155 160

His Tyr Val Ser Arg His Lys Phe Thr Gly Val Asn Gln Leu Thr Ile
165 170 175

Phe Ile Glu Asp Ile Tyr Asp Glu Gly Glu Glu Glu Cys His Leu His
180 185 190

Ser Ile Glu Leu Arg Gly Glu Phe Thr Glu Leu Asn Lys Asp Pro Val
195 200 205

Ile Thr Leu Tyr Glu Ser Ala Ala Asn Pro Ala Asp His Lys Asn Leu
210 215 220

Thr Ile Val Glu Asn Gln Asn Leu Ala
225 230

<210> 52
<211> 1833
<212> DNA
<213> Candida albicans

<400> 52
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gatgaagatg aactcgatcc cgaagagttc attttaaata aagtagataa accagctaca 180
aaagactcac atgtgctgta caataaattt ctggataagc atataagtga tgagcaacta 240
tcacacttac tcgacaatca taaacccaat ctagtgacta ccacaacttt aattgattct 300
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agtgacacca agctgactac aaaaatggaa taa 1833

<210> 53
<211> 610
<212> PRT
<213> Candida albicans

<400> 53
Met Ala Ser Ser Asn Asn Gly Phe Glu Ser Ile Asn Leu Ala Ser Thr
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Ile Ser Gly Pro Tyr Gln Glu Glu Asp Thr Pro Ile Lys Arg Leu His
20 25 30

Ser Ile Pro Ala Ser Thr Ser Glu Asp Glu Asp Glu Leu Asp Pro Glu
35 40 45

Glu Phe Ile Leu Asn Lys Val Asp Lys Pro Ala Thr Lys Asp Ser His
50 55 60

Val Ser Tyr Asn Lys Phe Ser Asp Lys His Ile Ser Asp Glu Gln Leu
65 70 75 80

Ser His Leu Leu Asp Asn His Lys Pro Asn Leu Val Thr Thr Thr Thr
85 90 95

Leu Ile Asp Ser Ile Lys Glu Ser Glu Ser Leu Tyr Asn Thr Met Asp
100 105 110

Ser Leu Met Ile Lys Ser Ile Asn Phe Pro Ala Ala Met Tyr Gln Ser
115 120 125

Asn Asp Asn Asn Ser Gln Ser Pro Ile Glu Tyr Leu Ser Asn Arg Val
130 135 140

Lys Leu Leu Thr Gln Glu Leu Tyr Glu Asp Ser Val Lys Tyr Gly Lys

145 150 155 160

Phe Leu Gln Ser Gly Asn Asn His Ile Tyr Gln Leu Arg Ser Arg Ile
165 170 175

Leu Gln Thr Phe Asp Gln Leu Ser Glu Ser His Tyr Ser Leu Asn Glu
180 185 190

Leu Tyr Asn Lys Asp Met Ser Tyr Ala Glu Thr Leu His Gly Ser Phe
195 200 205

Lys Lys Trp Asp Gln Gln Arg Asn Lys Val Leu Ser Lys Val Lys Ser
210 215 220

Ile Lys Ser Asp Thr Ser Lys His Gly Ala Lys Leu Phe Thr Leu Leu
225 230 235 240

Asp Glu Val Asn Asp Val Asp Asp Glu Ile Lys Leu Leu Glu Ala Lys
245 250 255

Leu Gln Gln Leu Arg Ser Lys Lys Glu Ile Leu Asn Lys Glu Ile Glu
260 265 270

Asp Thr Ser Ser Val Leu Glu Ser Arg Thr Ala Lys Tyr Val Asp Ile
275 280 285

Phe Lys Asp Leu Glu Asn Lys Gly Arg Ser Ala Ile Thr Asp Phe Leu
290 295 300

Gln Ser Asn Gly Val Pro Glu Lys Glu Ile Asp Thr Ile Val Arg Phe
305 310 315 320

Ser Pro Val Asp Ile Thr Ile Ser Ser Asn Tyr Ser Ser Lys Lys Glu
325 330 335

Pro Lys Lys Glu Ile His Ile Thr Lys Glu Ser Ile Pro Gln Asn Glu
340 345 350

Ser Ala Ser Lys Pro Ala Asn Thr Pro Ser Ile Gly Met Gln Pro Phe
355 360 365

Ile Ile Pro Glu Ala Glu Ala Asn Thr Lys Thr Pro Asp Leu Gln Ser
370 375 380

Met Asn His Asp His Gly Pro Thr Pro Phe Glu Lys Gly Tyr Ala Met
385 390 395 400

Gly Thr Gln Asn Ser Thr Ala Leu Lys Asn Lys Met Asn His Ile Met

405 410 415

Lys Lys Phe Leu Asp Ser Leu Pro Ile Thr Pro Pro Ser Asn Ile Ser
420 425 430

Thr Met Pro Ala Thr Ser Arg Ile Lys Val Asp Asp Leu Ser Asn Thr
435 440 445

Ile Ser Lys Arg Leu Asp Leu Asp Pro Ile Met Val Phe Leu Glu His
450 455 460

Lys Val Ala Ala Leu His Asp Leu Ala Ile Lys Ser Ser Gln Asn Ala
465 470 475 480

Ala Leu Phe His Glu Phe Gly Arg Ile Trp Glu Ser Val Thr Lys Leu
485 490 495

Met Asn Ser Gln Glu Glu Lys Leu Glu Ser Ile Leu Asn Asp Asp Ser
500 505 510

Asn Ser Lys Leu Val Thr Arg Ile Leu Asn Ser Thr Leu Glu Gln Leu
515 520 525

Lys Ser Thr Leu Ser Ala Leu Lys Ser Asn Pro Val Thr Ser Gly Ser
530 535 540

Pro Arg Asp Glu Val Leu Ile Ser Leu Ile Thr Ser Glu Tyr Asn Ala
545 550 555 560

Ile Glu Gln Ala Val Lys Leu Val Ser Pro Asp Leu Arg Thr Ile Gly
565 570 575

Glu Leu Asn Ser Ser Gly Gly Leu Pro Pro Ser Ser Ser Lys Pro Thr
580 585 590

Ser Gln Val Tyr Pro Val Ser Thr Ser Asp Thr Lys Ser Thr Thr Lys
595 600 605

Met Glu
610

<210> 54
<211> 75
<212> PRT
<213> Candida albicans

<400> 54

Met Ser Thr Tyr Phe Ala Val Ser Leu Ser Lys Thr Ser Ser Val Ser
1 5 10 15

Ser Ile Ser Leu Phe Lys Ile Ser Phe Leu Asp Arg Ser Cys Cys Ser
20 25 30

Phe Ala Ser Lys Ser Leu Ile Ser Ser Ser Thr Ser Leu Thr Ser Ser
35 40 45

Asn Lys Val Asn Asn Leu Ala Pro Cys Leu Leu Val Ser Leu Phe Ile
50 55 60

Asp Phe Thr Leu Asp Asn Thr Leu Phe Leu Cys
65 70 75

<210> 55
<211> 1164
<212> DNA
<213> Candida albicans

<400> 55
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ttggtgctgg acttgagtcg taatctaggc attgatagtc gagattttcc atatgaatta 180
cctgggaaac ggatcaactg gcttaacaag accagtattg ttgaggagag aaaagtggga 240
cttgcagaat ttctcaataa cctcattcaa gactcaacac ttcagaatga acgagaagtg 300
ttgtcgtttt tgcaattgcc gtctaatttt agattcacca aggatatgtt acagaataat 360
cgagcagact tggattctgt gcaaaataac tggtacgatg tatatcgtaa gttgaaactg 420
gatatactca acgaatcgtc tagcagcatt agtgaacaga tacatattcg tgatcgcatt 480
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<210> 56
<211> 297
<212> PRT
<213> Candida albicans

<400> 56

Met Ser Thr Ile Thr Ile Pro His Asp Ile Glu Ile Gly Gly Ser Thr
1 5 10 15

Tyr Tyr Gln Ile Asn Ile Lys Leu Pro Leu Arg Ser Phe Thr Ile Lys
20 25 30

Lys Arg Tyr Ser Glu Phe Gln Gln Leu Val Ser Asp Leu Ser Arg Asn
35 40 45

Leu Gly Ile Asp Ser Arg Asp Phe Pro Tyr Glu Leu Pro Gly Lys Arg
50 55 60

Ile Asn Trp Leu Asn Lys Thr Ser Ile Val Glu Glu Arg Lys Val Gly
65 70 75 80

Leu Ala Glu Phe Leu Asn Asn Leu Ile Gln Asp Ser Thr Leu Gln Asn
85 90 95

Glu Arg Glu Val Leu Ser Phe Leu Gln Leu Pro Ser Asn Phe Arg Phe
100 105 110

Thr Lys Asp Met Leu Gln Asn Asn Arg Ala Asp Leu Asp Ser Val Gln
115 120 125

Asn Asn Trp Tyr Asp Val Tyr Arg Lys Leu Lys Ser Asp Ile Leu Asn
130 135 140

Glu Ser Ser Ser Ser Ile Ser Glu Gln Ile His Ile Arg Asp Arg Ile
145 150 155 160

Ser Arg Val Tyr Gln Pro Arg Ile Leu Asp Leu Val Arg Ala Ile Gly
165 170 175

Thr Asp Lys Glu Glu Ala Leu Lys Lys Lys Gln Leu Val Ser Gln Leu
180 185 190

Gln Glu Ser Ile Asp Asn Leu Leu Val Gln Glu Val Pro Arg Ser Lys
195 200 205

Arg Val Leu Gly Gly Ala Val Lys Glu Thr Pro Glu Thr Leu Pro Leu
210 215 220

Asn Asn Lys Glu Leu Leu Gln His Gln Val Gln Ile His Gln Asn Gln
225 230 235 240

Asp Lys Glu Leu Asp Gln Leu Arg Val Leu Ile Ala Arg Gln Lys Gln
245 250 255

Ile Gly Glu Leu Ile Asn Ala Glu Val Glu Glu Gln Asn Glu Met Leu
260 265 270

Asp Arg Phe Asn Glu Glu Val Asp Tyr Thr Ser Ser Lys Ile Lys Gln
275 280 285

Ala Arg Arg Arg Ala Lys Lys Ile Leu
290 295

<210> 57
<211> 7707
<212> DNA
<213> Candida albicans

<400> 57
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gaactaagac aaaccgctat tatcactccg tctgagaaca agactataat agagtattta 480
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Leu Thr Gly Phe His Leu Ser Thr Ile Thr Ile Asn Asn Gly Ile Ser
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Phe Asn Gly Ile Ser Phe His Thr Lys Arg Tyr Leu Ile Ser Val Gly
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Ser Leu Arg Phe Arg Leu Trp Gly Asn Ser Lys Met Thr Ile Ile Asp
65 70 75 80

Asp Leu Thr Ile Lys Leu Leu Pro Asn Val Lys Asn Asn Gln Lys Gln
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Asn Thr Gln Glu Lys Arg Asn Asp Tyr Ser Phe Lys Asp Pro Thr Ala
100 105 110

Pro Val Val Asn Ile Phe Pro Gln Asn Arg Ile Gly Lys Tyr Val Val
115 120 125

Ser Arg Leu Ile Arg His Leu Pro Lys Met Asn Leu Glu Leu Arg Gln
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Thr Ala Ile Ile Thr Pro Ser Glu Asn Lys Thr Ile Ile Glu Tyr Leu
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Lys Phe Thr Thr Ser Ser Lys Tyr Ser Lys Arg Ser Asn Glu Lys Ile
165 170 175

Thr Phe Lys Ala Gly Leu Tyr Ile Asn Asn Val Leu His His Leu Lys
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Thr Asn Asn Gln Ser Thr Leu Ser Gln Ala Glu Ile Glu Ala Lys Glu
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Glu His Lys Leu Gln Arg Leu Glu Asn Thr Phe Lys Ile Ile His Ala
        275                 280                 285

Ile Val Ser Glu Ile Asn Leu His Ile Glu Asn Val Lys Ile Ser Glu
    290                 295                 300

Ile Pro Phe Val Thr Met Glu Asn Asn Pro Asp Phe Lys Glu Tyr Phe
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Asn Asp Val Arg Pro Ala Thr Cys Leu Glu Met Met Thr Lys Ser Thr
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Ser Phe Asn Phe Ser Arg Met Tyr Ser Asp Ala Ala Gly Phe Glu Val
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Leu Phe Asn Ser Lys Arg Asp Arg Pro Tyr His Leu Thr Cys Ser Val
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Gln Leu Leu Lys Val Phe Phe Ala Ser Arg Val Glu Leu Pro Thr Gly
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385                 390                 395                 400

Leu Thr Tyr Lys Thr Asn Ile Leu Asn Gln Val Val Arg Ala Arg Gly
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Phe Lys Asn Cys Val Val Glu Ile Tyr Phe Ser Ala Ser Thr Pro Ile
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Leu Asp Leu Asp Thr Arg Gln Leu Ser Ser Leu Leu Tyr Asn Leu Val
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Ser Glu Thr Ser Asn Leu Lys Ile His Pro Gly Thr Pro His His Lys
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His Leu Asp Ile Lys Thr Val Val Glu Gln Pro Arg Leu Val Leu Arg
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His Cys Glu Pro Lys Lys Asn Thr Gln Ile Leu Thr Phe Ser Tyr Ser
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Ser Cys Gln Leu Leu Leu Pro Leu Val Thr Tyr Tyr Glu Lys Pro Phe
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Ser Asp Val Ser Asp Leu His Gly Lys Glu Leu Val Thr Lys Arg Val
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Ala His Thr Ser Tyr Ile Asp Ile Lys Leu Glu Ile Phe Lys Asn Leu
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Thr Val Lys Leu Leu Val Asp Val Asp Lys Val Thr Ile Asp Leu Thr
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Asn Leu Asp Ile Phe Thr Gly Ile His Asn Leu Leu Leu Asp Val Thr
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Gln Ile Ala Glu Thr Asp Leu Glu Leu Gly Val Ile Asn Lys Met Leu
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Asn Leu Gln Phe Leu Gln Leu Arg His Glu Leu Gln Leu Arg Gln Val
660 665 670

Ser Tyr Phe Lys Lys Asn Ile Lys Pro Thr Leu Glu Gln Lys Leu Phe
675 680 685

Arg Tyr Leu Pro Lys Trp Leu Thr Arg Ile Asp Leu Lys Val Thr Phe
690 695 700

Leu Asn Ile Ser Leu Gly Ser Arg Ser Val Leu Ile Pro Lys Lys Asp
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Leu Ser Arg Ala Glu Ser Pro Asp Phe Asp Phe Asp Phe Asp Asp Asp
725 730 735

His Glu Leu Lys Gln Ile Asp Leu Lys Phe Asp Ser Leu Ser Ile Gly
740 745 750

Val Ala Lys Asn Ser Lys Thr Ser Gly Glu Ser Thr Pro Ser Thr Val
755 760 765

Ala Ser Ser Ala Ser Ser Glu Thr Leu Thr Ile Ser Asn His Asp Thr
770 775 780

Val Tyr Trp Ala Val Asn Ala Thr Leu Glu Lys Leu Lys Leu Ser Ala
785 790 795 800

Leu Thr Asp Leu Asp Gly Lys Phe Gly Arg Leu Leu Glu Ile Pro Thr
805 810 815

Ile Lys Thr Asn Val Ser Ala Ile Cys Asp Tyr Tyr Gly Asn Asn Lys
820 825 830

Leu Ile Thr Asp Val Lys Val Glu Lys Ile Leu Val Asp Tyr Asn Arg
835 840 845

Tyr Lys Leu Tyr Thr Leu Ile Gly Ser Ile Tyr Leu Ile Arg Glu Phe
850 855 860

Val Leu Ala Pro Ile Lys Val Ile Lys Ser Lys Val Asn Lys Asp Leu
865 870 875 880

Thr Lys Phe Asp Ser Asn Leu Ser Pro Asp Pro Asn Ala Ala His Lys
885 890 895

Thr Thr Ser Ile Leu Asp Phe Leu His Leu Asp Phe Lys Leu Asp Tyr
900 905 910

Ser Asp Met Ile Leu Cys Leu Ser Lys Asp Phe Lys Val Arg Leu Gln
915 920 925

Leu Asn Ala Met Gln Ala Ala Tyr Arg Asp Arg Thr Ala Asp Leu Ser
930 935 940

Ile Thr Phe Leu Arg Gly Leu Ala Glu Ser Pro Leu Val Ala Asn Lys
945 950 955 960

Trp Cys Arg Leu Leu Cys Leu Asp Thr Leu Lys Phe Lys Ser Glu Ile
965 970 975

Thr Ser Ser Ile Lys Asp Leu Ser Ile Glu Leu Asp Ser Asp Ala Val
980 985 990

Arg Phe Ile Gln Pro His Gln Phe Val Val Tyr Lys Phe Phe Asp Asn
995 1000 1005

Ile Ser Ile Thr Val Lys Leu Val Lys His Leu Val Lys Leu Leu Lys
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Asp Glu Ser Thr Lys Glu Asp Leu Asn Ile Val His Pro Asn Leu Gln
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Lys Ala Lys Leu Leu Pro Phe Ile Arg Phe Lys Ser Lys Ser Leu Lys
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Phe Cys Val Glu Asp Asp Pro Phe Glu Thr Glu Leu Gly Met Ile Tyr
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Gln Leu Gly Lys Val Glu Gln Arg Lys Arg Leu Glu Leu Tyr Asn Leu
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Phe Glu Thr Lys Ala Ser Thr Ser His Ile Asp Thr Glu Glu Tyr Phe
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Asp Asn Leu Ser Arg Leu Asn Arg Thr Ile Ser Gln Ser Trp Ile Arg
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Lys Val Asn Val Tyr Lys Ser Lys Leu Arg Ser Glu Ile Ile Ala Asn
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Lys Asp Tyr Leu Leu Gly Asn Glu Val Lys Leu Asp Glu Ser Leu Asn
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Asp Asp Val Val Thr Tyr Ala Tyr Ala Ser Pro Leu Phe Ser Val Tyr
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Glu Leu Arg Met His Leu Arg Asp Tyr Pro Leu Pro Leu Leu His Ser
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Pro Arg Asn Lys Asp Met Asp Glu Thr Ser Phe Lys Leu Asn Gly His
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Leu Val Ile Ser Glu Ala Phe Ala Lys Ala Ile Glu His Met Arg Gln
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Ile Asp Val Pro Leu Val Pro Glu His Lys His Lys His Lys Gln Leu
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Leu Cys Thr Asp Leu Glu Cys Val Phe Asn Ser Asn Tyr Pro Thr Arg
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Ile Val Trp Gly Ala Ser Tyr Asn Phe Gly Ile Gln Gln Met Met Ala
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Gly Phe Trp Asp Lys Leu Lys Tyr Ile Leu His Gly Lys Cys Gln Ile
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Arg Thr Arg Lys Ser Leu Glu Val Ala Phe Lys Gly Ser Arg Asp Pro
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Tyr Asp Leu Phe Thr Thr Ala Gly Gly Phe Val Leu Ser Phe Arg Lys
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Asp Ile Thr Ala Asp Lys Val Ser Trp Tyr Ile Pro Asn Tyr Leu Ala
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Gly Pro Leu Leu Ala Trp Thr Arg Ser Ser Lys Asn Ser Ile Tyr Leu
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Pro Asn Ser Pro Asn Val Val Asn Ser Cys Phe Ala Tyr Tyr Leu Gln
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Asp Phe Thr Gly Gln Ala Asp Phe Asp His Ala Ala Arg Val Phe Glu
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Arg Asn Val Val Asn Leu Ser Gly Gly Ile His Phe Gln Val Gly Phe
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Leu Leu Glu Arg Lys Asp Thr Asn Gly Lys Arg Thr Asp Glu Phe Lys
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Pro His Tyr Glu Val Gln Leu Phe Asp Pro Lys Tyr Cys Glu Lys Gly
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His Asp Ser Tyr Ala Gly Phe Arg Ser Gln Phe Ile His Met Ala Ile
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Ser Leu Glu Ser Thr Asn Ser Ser Ser Tyr Asn Thr Ile His Leu Ser
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Pro Gly Thr Phe Gln Gln Phe Phe Asp Trp Trp Lys Leu Phe Ala Ser
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Asn Met Gln Leu Pro Ile Arg Arg Gly Lys Met Phe Gly Glu Ala Lys
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Glu Ser Val Lys Phe Ser Gln His Leu Phe Thr Asn Lys Phe Ser Phe
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Met Leu Lys Ser Leu Phe Ile Ala His Val Tyr Arg Asp Glu Ile Val
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Asp Ile Asn Asn Asp Arg Ile Glu Ser Ile Gly Leu Arg Ala Lys Val
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Asp Asp Phe Met Val Asp Leu His Gln Arg Lys Glu Pro Ala Thr Leu
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Tyr His Glu Glu Leu Ser Lys Asn Glu Lys Val Met Lys Met Asn Phe
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Asp Leu Gly Glu Val Val Leu Ser Gly Ile Asp Leu Arg Val Met His
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Val Ser Phe Leu Gln Asn Leu Tyr Thr Gln Ser His Ser Asn Ser Gly
1685 1690 1695

Asp Ala Lys Ser Thr Tyr Asn Ile Tyr Asp Asn Asp His Arg Trp Phe
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Asp Ile Met Asp Phe Gln Glu Ala Phe Leu Thr Ser Ile Lys Asp Cys
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Val Arg Thr Val Asp Ile Tyr Pro Leu Met Tyr Leu Gln Arg Phe Phe
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Tyr Glu Arg Asp Thr His Gly Gly Lys Ser Glu Asp Glu Thr Ala Phe
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Gly Lys Glu Val Ile His Lys Cys Asn Leu Gly Ala Met Asn Pro Leu
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Glu Thr Arg Leu Asn Val Leu Val Gln Arg Leu Asn Ala Leu Gln Glu
1780 1785 1790

Gln Val Lys Lys Leu Ser Lys Thr Ser Ala Pro Glu Pro Val Ala Asp
1795 1800 1805

Leu Lys Lys Arg Ile Ser Phe Leu Gln Lys Glu Ile Ser Thr Thr Lys
1810 1815 1820

Ala Ser Val Lys Ser Lys Met Arg Arg Thr Ser Thr Ile Asn Gly Met
1825 1830 1835 1840

Asn Asn Ser Glu Asn Tyr His Asn Lys Phe Thr Phe Tyr Asn Met Leu
1845 1850 1855

Leu Lys Trp Asn Phe Asn Cys Arg Asn Leu Thr Leu Lys Tyr Ile His
1860 1865 1870

Phe Val Lys Leu Lys Ser Gln Leu Arg Asn Tyr Leu Ser His Lys Ser
1875 1880 1885

Ile Glu Thr Leu Glu Lys Met Met Asp Ser Val Asn Ala Tyr Asn Asp
1890 1895 1900

Lys Asp Asp Leu Ser Ser Thr Ser Glu Ile Ile Arg Arg Phe Thr Ser
1905 1910 1915 1920

Glu Gly Val Lys Ser Gln Thr Ser Thr Ser Lys Asp Ile Thr Ser Gln
1925 1930 1935

Gln Lys Leu Asp Asn Phe Asn Thr Ile Leu Arg Glu Thr Arg Pro Asp
1940 1945 1950

Glu Lys Val Val Glu Asp Tyr Leu Ile Asp Val Ile Ala Pro Gln Ile
1955 1960 1965

Gln Leu Gln Ser Glu Asp Tyr Pro Asp Ser Val Val Leu Ile Ser Thr
1970 1975 1980

Pro Ser Ile Lys Gly Lys Ile Leu Ser Ile Met Asp Ser Arg Asn Asn
1985 1990 1995 2000

Ala Asn Gln Ile Leu Leu Glu Thr Arg Tyr Gly Ile Leu Leu Lys Asp
2005 2010 2015

Ala Asn Val Phe Val Leu Asn Lys Glu Asp Ile Val Gly Cys Pro Asp
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Met Leu Ser Ile Ser Asn Pro Tyr Gly Ala Lys Ser Asn Trp Pro Pro
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Glu Ile Leu Ser Ser Lys Leu Ser Pro Asn Ala Gln Asp Ser Asp Gln
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Glu Glu Gln Glu Asn Tyr Asn Asp Asp Asn Ser Lys Gln Ala Pro Leu
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Gln Tyr Phe Thr Leu Tyr Val Ile Ile Val Ser Leu Leu Phe Tyr Ser
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Glu Asp Asp Arg Thr Pro Ile Met Asp Leu Ala Leu Ala Gln Gly Met
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Tyr Thr Arg Lys Glu Leu Glu Ser Gly Ser Asn Ile Asn Lys Leu His
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Met Ala Ser Ile Ser Val Pro Ile Glu Lys Gly Ser Phe His Asp Gly
1 5 10 15

Asp Gly Phe Asn Gln His His Leu Gly Asp Pro Val Ile Ser Gly Pro
20 25 30

Pro Tyr Ile Ile Lys Leu Leu Asn Leu Pro Val Thr Ala Asn Asp Ser
35 40 45

Phe Val Gln Asp Leu Phe Gln Ser Arg Phe Thr Pro Tyr Val Lys Phe
50 55 60

Lys Ile Val Thr Asp Pro Ala Ser Asn Ile Leu Glu Thr His Val Ile
65 70 75 80

Arg Gln Val Ala Phe Val Glu Leu Glu Ser Ala Ser Asp Met Ser Lys
85 90 95

Ala Leu Lys Trp His Asp Leu Tyr Tyr Lys Thr Asn Arg Arg Val Thr
100 105 110

Val Glu Val Ala Asp Phe Asn Asp Phe Gln Asn Cys Ile Lys Phe Asn
115 120 125

Gln Glu His Glu Arg Glu Ile Met Gln Ile Gln Gln Glu Phe Ile Ala
130 135 140

Gln Lys Gln Gln Gln Arg Gln Pro Arg His Met Ala Leu Leu Asp Glu
145 150 155 160

Phe Glu Arg Asn Gln Arg Gly Pro Gly Ser Pro Leu His Gln Asn His
165 170 175

Asp His His Asn Pro His Pro Gln Gln Gln Gln His His His Phe Asn
180 185 190

Pro Asn Leu Asn Arg Pro Ser Gly Arg Ser Ser Leu Pro Ile Asp Glu
195 200 205

Thr Ser His Ser Arg Arg Leu Ser Phe Glu Ala Gln Leu His Pro His
210 215 220

Gln Gln Thr His Gly Gln Arg Ile Arg Gln Pro Ser Phe Asp Asn Ala
225 230 235 240

Phe Pro Asp Thr Pro His Pro Pro Phe Gly Gly Gly Gly Gly Met Arg
245 250 255

Gln Gln Ile His Pro Thr Asn Gln Pro Ala Val Pro Ser Ser Ala Pro
260 265 270

Ala Ser Lys Pro Phe Val Thr Pro Ile Ser Ser Ala Ser Thr Ser Ser
275 280 285

Arg Pro Ile Ser Asn Pro Phe Gly Ala Ala Lys Pro Val Asp Thr Leu
290 295 300

Ser Lys Gln Gln Glu Ile Glu Lys Lys Leu Ile Asn Leu Asn Lys Thr
305 310 315 320

Thr Val Gln Thr Leu Gly Asp Val Glu Thr Pro Glu Glu Val Gln Ala
325 330 335

Thr Ile Lys Lys Phe His Glu Asn Gly Ser Pro Lys Leu Arg Arg Ala
340 345 350

Ser Val Gly Thr Pro Arg Arg Leu Ser Ser Glu Lys Arg Pro Ser Val
355 360 365

Ser Ile Leu Arg Arg Asp Leu Pro Glu Arg Gln Gln Pro Pro Pro Pro
370 375 380

Pro Gln Gln Gln Gln Gln Gln Gln Pro Pro Gln Gln Gln Asp Gln Asn
385 390 395 400

Thr Lys Gln Thr Ala Leu His Gln Pro Asp Gln Leu Gln Asn His Ser
405 410 415

Ser Asn Ile Ser Ser Thr Gln Pro Ser Gly Glu Ser Pro Leu Ala Glu
420 425 430

Thr Gln Ser Leu Ser Thr Asn Pro Tyr Thr Ser Asn Gly Thr Gly Lys
435 440 445

Ser Leu Ala Gln Leu Leu Ser Glu Gln Ser Asp Ile Met Ser Ala Pro
450 455 460

Pro Ile Thr Gly Lys Lys Thr Pro Arg Ser Asn Ser Asn Thr Lys Lys
465 470 475 480

Pro Val Val Ala Ala Lys Pro Val Ile Leu Lys Lys Lys Thr Pro Thr
485 490 495

Ser Pro Pro Val Gln Arg Ile Asp Leu Thr Ile Lys Glu Ser Glu Tyr
500 505 510

Leu Lys Lys Gln Asp Glu Thr Asp Asp Leu Ile Asp Ala Asn Val Glu
515 520 525

Thr Lys Leu Glu Lys Leu Asp Leu Asn Ser Glu Thr Leu Ser Glu Asn
530 535 540

Gly Thr Lys Glu Ser Thr Lys Thr Arg Ile Asp Asn Pro Lys Arg Glu
545 550 555 560

Asn Asp Gln His Asp Asp Arg Pro Asn Phe Lys Asn Leu Asp Gln Leu
565 570 575

Val Gln Lys Arg Asn Asp Ser Arg Ala Ser Ser Ser Ser Ser Asn Ser
580 585 590

Arg Arg Phe Glu Phe Ile Arg Gly Leu Lys Glu Glu Asn Glu Arg Val
595 600 605

Pro Ser Pro Ser Ser Ser Ser Ser Ser Ser Ser Ala Thr Lys Thr Ser
610 615 620

Gln Asn Asn Phe Glu Lys Ser Ser Glu Ser Ala Ile Ser Arg Thr Asp
625 630 635 640

Asp Gln Gln Asp Leu Ser Ser Thr Asn Thr Gly Ser Glu Gly Arg Met
645 650 655

Trp Glu Arg Gly Arg Gly Arg Gly Arg Gly Gly Phe Ser Phe Arg Ser
660 665 670

Arg Gly Gly Phe Arg Gly Arg Gly Ala Gly Phe Arg Gly Ser Gly Arg
675 680 685

Gly Gly Pro Arg Arg Arg Gly Gly Asn Gly Ala Ser Gly Ala Gly Gly
690 695 700

Thr Ala Ser Gly Ser Thr Gly Ser Ala Asn Tyr Asn Leu His Tyr Val
705 710 715 720

Arg Ser Lys Pro Thr Pro Val Glu Thr Asn Glu
725 730

<210> 61
<211> 1483
<212> DNA
<213> Candida albicans

<400> 61
gtagtttgtg aagaaattga aacaatcgga aaacaacaat atcaaactga tgcccaataa 60
cactgtatgt acctagatgg attaccaaga tctactacat aaaataataa aggagttcca 120
ctcactcaaa gagttcaaac catgggatag cagtgttttg tatgagacgt tactacgatc 180
agtattaact actttgatcg aacttttggg catagacaat ccacccagtt atctacacct 240
caccaccaac aatgatagta taggtgattt gaaaataaaa tactatggaa atgcattaag 300
caagtcaatc aacggtcata gcatgttgca atatcttgaa tcaaagcatg tatcgatatt 360
acaggccgtg gttgagatta ttaatacgcg atcatataga atcaaagagt cttattctgc 420
tgttttcaaa gacgtttctc atttatttga aaaactacta aaggaaagat atgaagctga 480
atctaatcta gaggattata tattgcagtg cttgatgtac gagacccaat tttaccaagg 540
aattgttgat aatgttttaa ctgccgatga caccgaaaaa ttggctagtt ttttggggac 600
acgactatct gaagaagatt cgatgtttag ctatagggat atagattatc cactagagtt 660
aaacattaat aatgaatctc ttgaaaagat atataaaatt ttcttaggag tcattggcac 720
caaaagattc gatatcaagg aggttgcgtc tgctgttgtt ggtgtgtata aacgacacca 780
gagaatagat cattttgaaa agttggattc agatgagatt ttgggaaagt ttttcagaaa 840
tatattgcca caactgttcc agagtgtgac aaataaggtt ttccgggaat ttcacaaaga 900
ggtagatgac ccaccatcgg acgtgctaga ccagctagat aatattgttg atgactttat 960
tgcggttgga attgaagggg tagatttggg ctttccggct ttgttcagac actacataaa 1020
attcatgaac gaaatttttc ccactgtggt cgaggatgct gaccgcgatt ttgttgcaag 1080
aattaatagt ttaattgctc aagtcttgga gtttaaagac gatgaaaaat cctgtgatat 1140
caatcaagtg gtatctgaat ttgtttcatt acaaagtttg ctacttaaga ataactatct 1200
ttcaccatct acattattga tgcgtgcaag tactcacgat tactataaaa atttacagat 1260
cgtgaaaata acctttgatg gatggaatga gaattcaaag aggatattga aattggagaa 1320
cagcggcttt ttacaaagca agacattgcc aaagtattta aaattatggt actcaaaaag 1380
tatgaagttg aatgaattat gtaaccgggt agatgaattt tataatggag aactttgtcg 1440
gaaagtttgg cattgttgga gggcacaaca aagatgtcta taa 1483

<210> 62
<211> 468
<212> PRT
<213> Candida albicans

<400> 62

Met Asp Tyr Gln Asp Leu Leu His Lys Ile Il Lys Glu Phe His Ser
1 5 10 15

Leu Lys Glu Phe Lys Pro Trp Asp Ser Ser Val Leu Tyr Glu Thr Leu
20 25 30

Leu Arg Ser Val Leu Thr Thr Leu Ile Glu Leu Leu Gly Ile Asp Asn
35 40 45

Pro Pro Ser Tyr Leu His Leu Thr Thr Asn Asn Asp Ser Ile Gly Asp
50 55 60

Leu Lys Ile Lys Tyr Tyr Gly Asn Ala Leu Ser Lys Ser Ile Asn Gly
65 70 75 80

His Ser Met Leu Gln Tyr Leu Glu Ser Lys His Val Ser Ile Leu Gln
85 90 95

Ala Val Val Glu Ile Ile Asn Thr Arg Ser Tyr Arg Ile Lys Glu Ser
100 105 110

Tyr Ser Ala Val Phe Lys Asp Val Ser His Leu Phe Glu Lys Leu Leu
115 120 125

Lys Glu Arg Tyr Glu Ala Glu Ser Asn Leu Glu Asp Tyr Ile Leu Gln
130 135 140

Cys Leu Met Tyr Glu Thr Gln Phe Tyr Gln Gly Ile Val Asp Asn Val
145 150 155 160

Leu Thr Ala Asp Asp Thr Glu Lys Leu Ala Ser Phe Leu Gly Thr Arg
165 170 175

Leu Ser Glu Glu Asp Ser Met Phe Ser Tyr Arg Asp Ile Asp Tyr Pro
180 185 190

Leu Glu Leu Asn Ile Asn Asn Glu Ser Leu Glu Lys Ile Tyr Lys Ile
195 200 205

Phe Leu Gly Val Ile Gly Thr Lys Arg Phe Asp Ile Lys Glu Val Ala
210 215 220

Ser Ala Val Val Gly Val Tyr Lys Arg His Gln Arg Ile Asp His Phe
225 230 235 240

Glu Lys Leu Asp Ser Asp Glu Ile Leu Gly Lys Phe Phe Arg Asn Ile
245 250 255

Leu Pro Gln Ser Phe Gln Ser Val Thr Asn Lys Val Phe Arg Glu Phe
260 265 270

His Lys Glu Val Asp Asp Pro Pro Ser Asp Val Leu Asp Gln Leu Asp
275 280 285

Asn Ile Val Asp Asp Phe Ile Ala Val Gly Ile Glu Gly Val Asp Leu
290 295 300

Gly Phe Pro Ala Leu Phe Arg His Tyr Ile Lys Phe Met Asn Glu Ile
305 310 315 320

Phe Pro Thr Val Val Glu Asp Ala Asp Arg Asp Phe Val Ala Arg Ile
325 330 335

Asn Ser Leu Ile Ala Gln Val Leu Glu Phe Lys Asp Asp Glu Lys Ser
340 345 350

Cys Asp Ile Asn Gln Val Val Ser Glu Phe Val Ser Leu Gln Ser Leu
355 360 365

Leu Leu Lys Asn Asn Tyr Leu Ser Pro Ser Thr Leu Leu Met Arg Ala
370 375 380

Ser Thr His Asp Tyr Tyr Lys Asn Leu Gln Ile Val Lys Ile Thr Phe
385 390 395 400

Asp Gly Trp Asn Glu Asn Ser Lys Arg Ile Leu Lys Leu Glu Asn Ser
405 410 415

Gly Phe Leu Gln Ser Lys Thr Leu Pro Lys Tyr Leu Lys Leu Trp Tyr
420 425 430

Ser Lys Ser Met Lys Leu Asn Glu Leu Cys Asn Arg Val Asp Glu Phe
435 440 445

Tyr Asn Gly Glu Leu Cys Arg Lys Val Trp His Cys Trp Arg Ala Gln
450 455 460

Gln Arg Cys Leu
465

<210> 63
<211> 715
<212> DNA
<213> Candida albicans

<400> 63
tgtttggttg taatagtatt tctatattac atttcacttt tgaagacaaa agaattttta 60
ggtacaaaat tgttgccaaa attttataaa aaattgtcaa atgaaaagaa gtatttccaa 120
atatattgtt tttcatcaca acagttcata tcgccataga ccatttttaa tcttaaggtt 180
gataccagtt aattgttgat ttctctgtta tagaccctgt ctaaatctgt ctatttctgg 240
tatcgaatca aaatgtcgct cataatgtgc atgtcgcaaa gatgtcgtaa agttttgatt 300
tcatactcat cttaaatttt ttttagtgat tggcattttg ttctttcaca tagtttttat 360
ttctagttat caacctatca aatacacctc cacaacaatg catccaaata ataaaaattc 420
atttaaatca aaaaagaaat ttatagatcg tcgagaagcc aagtctcaag atataaaacg 480
tgcattaacc catagggcta gattaagaaa gaactatttc aaactattag aaaaagaagg 540
gttacaagag gagaggaagc ctgaagatga gaacgatata agaccaacca agaagaaggg 600
aataaatttt gaagaacgtg cagccattgt gaaacaacgt aaagaggaaa aacgtaaatt 660
caaactagca agtgtacaag caaaattgga aaagattgaa tctaattcga aagaa 715

<210> 64
<211> 106
<212> PRT
<213> Candida albicans

<400> 64
Met His Pro Asn Asn Lys Asn Ser Phe Lys Ser Lys Lys Lys Phe Ile
1 5 10 15

Asp Arg Arg Glu Ala Lys Ser Gln Asp Ile Lys Arg Ala Leu Thr His
20 25 30

Arg Ala Arg Leu Arg Lys Asn Tyr Phe Lys Leu Leu Glu Lys Glu Gly
35 40 45

Leu Gln Glu Glu Arg Lys Pro Glu Asp Glu Asn Asp Ile Arg Pro Thr
50 55 60

Lys Lys Lys Gly Ile Asn Phe Glu Glu Arg Ala Ala Ile Val Lys Gln
65 70 75 80

Arg Lys Glu Glu Lys Arg Lys Phe Lys Leu Ala Ser Val Gln Ala Lys
85 90 95

Leu Glu Lys Ile Glu Ser Asn Ser Lys Glu
100 105

<210> 65
<211> 147
<212> DNA
<213> Candida albicans

<400> 65

atgaagattt caccagagac agtaaataaa ctacaactgg atgcatcgtg tataagaaac 60
atctgtattt tagcacatgt cgaccacggt aaaacctcat tgagtgactc attattagcc 120
accaatggaa tcatttccca acgtatg 147

<210> 66
<211> 49
<212> PRT
<213> Candida albicans

<400> 66
Met Lys Ile Ser Pro Glu Thr Val Asn Lys Leu Gln Ser Asp Ala Ser
1 5 10 15

Cys Ile Arg Asn Ile Cys Ile Leu Ala His Val Asp His Gly Lys Thr
20 25 30

Ser Leu Ser Asp Ser Leu Leu Ala Thr Asn Gly Ile Ile Ser Gln Arg
35 40 45

Met

<210> 67
<211> 3393
<212> DNA
<213> Candida albicans

<400> 67
gtcatgcgat tgcaacaagg atcacaagaa ccagaagttc acgaacattt gattaatctg 60
attgattcac ctgggcatat tgacttttcg tctgaagtga gtacttcttc gagattatgt 120
gatggtgcag ttgttttggt cgatgtcgtc gaaggtgtct gctcacaaac agtcaacgtt 180
ctacgccaat gttggattga taagttgaag ccattactag ttattaacaa aattgatagg 240
ttaatcacag aatggaaatt gtctcccttg gaggcatacc aacacatttc cagaattata 300
gaacaagtaa actctgtgat tgggtcattt tttgctggtg atagactaga agatgacttg 360
aattggcgtg aggctggttc tgtcggggag tttatcgaga agagtgatga agacttgtat 420
ttcacacctg aaaagaataa tgtaatattt gcctcggcaa tagatggatg ggcattttca 480
gtcaatacat ttgccaaaat atacctgaaa aaattagggt tctctcaaca agcattgtca 540
aaaactctct ggggagactt ttacttggat atgaaaaata aaaaaatcat ccctggtaaa 600
aaattgaaaa ataatagtaa cagtttgaag ccattatttg tttcgttgat tttggaccag 660
gtttgggctg tttatgaaaa ctgtgttatt gaaagaaatc aagacaagtt ggaaaaaatc 720
attgagaaat taggggccaa aatcacccct cgtgatttgc gatccaaaga ttacaagaac 780
ttgctaaact tgattatgtc tcagtggatt cctttgagtc atgccatatt ggggtcagtg 840
attgaatact tgccaagccc cattgttgct cagcgtgaaa gaatagacaa gattttggat 900
gaaacgattt atagtgcagt ggattcagaa ctggataaat ccaaactagt cgacccttca 960
tttgtcaagg cgatgcagga atgtgatagt tcacacccgg aaacccatac aatagcatat 1020
gtatcaaaat tgttgtcaat ccccaatgaa gacttaccca aagctagtaa tgccgctact 1080
ggaggattga cggccgatga aatccaagaa cgaggaagaa ttgctcgaga attagccaaa 1140

aaggcatctg aagcagctgc tttggcacaa gaaggttcca aaaatgaaga tgagtttgcc 1200
attaaaccca agaaagatcc atttgaatgg gaatttgagg aggacgattt tgagaatgag 1260
gaagatgaga gcgatgcaaa cgcagttgaa gaatcaactg aaaccatagt gggtttcact 1320
cgtatttatt ctggatcgtt atctagaggc caaaagctca cggtaattgg acccaaatac 1380
gacccttcat tacctagaga ccatcaaacc aactttgaac aaataaccaa tgaagttgaa 1440
attaaagact tgtttttaat catgggacga gaattagtga gaatggaaaa agtcctgcgg 1500
gtaatattgt tggggttgtt ggattggata acgccgtgct taagaatgcc acaatttgct 1560
caccgttacc tgaagataaa ccatacatta atttagcttc aacatcaacc ttgatccaca 1620
ataaaccaat tatgaaaata gcagttgaac caacaaaccc aataaaacta gcaaaattgg 1680
aacgaggatt agatttattg gccaaagccg acccggtttt ggaatggtat gtcgacgacg 1740
agtcaggtga attgattgtt tgtgttgctg gagaattgca tctagaacga tgcttgaaag 1800
atttagaaga gagattcgct aagggttgtg aagttaccgt caaagagcca gtcattccct 1860
tcagagaggg gttggcagat gacaaaatca gtaccaacac caataataac aacgacgaca 1920
atgaagatca tgaattagat gaaaacgaag atgagcttgc tgatttagag tttgatattt 1980
ctccgttgcc attagaagtg actcagtttt taattgagaa tgaaacgatt attgccgaaa 2040
ttgtcaacaa caagcaagat actcatgaaa ttagaaacga ttttattgaa aaatttgcca 2100
ctattattga taattctaat ttggctacac aatttccaga caccaagtct tttatcaaca 2160
atataatttg ctttggacct aaacgtgttg ggcctaatat tttcattgaa gattatgggt 2220
taaacaaatt tagacatcta cttggtgaat ctgccactga atctcgattt gtttatgaga 2280
ataatgtgtt caatggggtt caattggtat tcaatggggg tccgttagca tcagagccaa 2340
tgcaaggtat tattgttaga cttaagaagg cagaaaaaag agaagttgac gaggataaaa 2400
tagtcaaccc tggtaaaata atcacacaga ctcgtgactt gatttacaag cggtttttgc 2460
aaaaatcacc acgcttgtac cttgcaatgt atacgtgtga aatccaagca gctgccgaag 2520
tgttgggtaa agtatatgct gttgttcaac gacgcgaagg gtcaatcata tcagaagaaa 2580
tgaaagaagg tactccgttc tttactattg tggcaagaat ccctgtgatt gaggcatttg 2640
ggttttccga ggatattaga aagaagacat ccggggcagc tagtcctcaa ttagtttttg 2700
atgggtatga tatgttagat atcgatccat tttgggttcc acatactgaa gaagaattag 2760
aagaattggg tgaatttgca gaaagagaaa atgttgctag aagatatatg aataatatca 2820
gaagaagaaa agggttattt gttgatgaga aagtcgtcaa aaatgctgaa aagcaaagaa 2880
ctttgaaaag agattagatt atccagtaaa acaggcaata tgtgtgaaat tgttacagaa 2940
aagacagata cgatgtggcc attatttgtt taatattcaa caacaagtaa atgtattgat 3000
atagatgtat aatatagtca aatgttgaga ctatccgaat agacatagac acacaactca 3060
gcctgtcagg gctgtttatt aagttgtgat gtatactaaa atccatccac acttctcgta 3120
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aatttgattg aaggtgttac tagtattgtt tcaacattac tcttttcaaa caacgagatc 3240
caaatactgc acaatcttca aacgaacgga gttacatcac tatagttttc tattgttgta 3300
agatcaatac agacaaaaag aaagtgtagc ataaataatt gattgcaatt tgccaaacta 3360
gaaaacaaag aggaaaaaaa gaaaaaaatt tca 3393

<210> 68
<211> 497
<212> PRT
<213> Candida albicans

<400> 68
Val Met Arg Leu Gln Gln Gly Ser Gln Glu Pro Glu Val His Glu His
1 5 10 15

Leu Ile Asn Ser Ile Asp Ser Pro Gly His Ile Asp Phe Ser Ser Glu
20 25 30

Val Ser Thr Ser Ser Arg Leu Cys Asp Gly Ala Val Val Leu Val Asp
35 40 45

Val Val Glu Gly Val Cys Ser Gln Thr Val Asn Val Leu Arg Gln Cys
50 55 60

Trp Ile Asp Lys Leu Lys Pro Leu Leu Val Ile Asn Lys Ile Asp Arg
65 70 75 80

Leu Ile Thr Glu Trp Lys Leu Ser Pro Leu Glu Ala Tyr Gln His Ile
85 90 95

Ser Arg Ile Ile Glu Gln Val Asn Ser Val Ile Gly Ser Phe Phe Ala
100 105 110

Gly Asp Arg Leu Glu Asp Asp Leu Asn Trp Arg Glu Ala Gly Ser Val
115 120 125

Gly Glu Phe Ile Glu Lys Ser Asp Glu Asp Leu Tyr Phe Thr Pro Glu
130 135 140

Lys Asn Asn Val Ile Phe Ala Ser Ala Ile Asp Gly Trp Ala Phe Ser
145 150 155 160

Val Asn Thr Phe Ala Lys Ile Tyr Ser Lys Lys Leu Gly Phe Ser Gln
165 170 175

Gln Ala Leu Ser Lys Thr Leu Trp Gly Asp Phe Tyr Leu Asp Met Lys
180 185 190

Asn Lys Lys Ile Ile Pro Gly Lys Lys Leu Lys Asn Asn Ser Asn Ser
195 200 205

Leu Lys Pro Leu Phe Val Ser Leu Ile Leu Asp Gln Val Trp Ala Val
210 215 220

Tyr Glu Asn Cys Val Ile Glu Arg Asn Gln Asp Lys Leu Glu Lys Ile
225 230 235 240

Ile Glu Lys Leu Gly Ala Lys Ile Thr Pro Arg Asp Leu Arg Ser Lys
245 250 255

Asp Tyr Lys Asn Leu Leu Asn Leu Ile Met Ser Gln Trp Ile Pro Leu
260 265 270

Ser His Ala Ile Leu Gly Ser Val Ile Glu Tyr Leu Pro Ser Pro Ile
275 280 285

Val Ala Gln Arg Glu Arg Ile Asp Lys Ile Leu Asp Glu Thr Ile Tyr
290 295 300

Ser Ala Val Asp Ser Glu Ser Asp Lys Ser Lys Leu Val Asp Pro Ser
305 310 315 320

Phe Val Lys Ala Met Gln Glu Cys Asp Ser Ser His Pro Glu Thr His
325 330 335

Thr Ile Ala Tyr Val Ser Lys Leu Leu Ser Ile Pro Asn Glu Asp Leu
340 345 350

Pro Lys Ala Ser Asn Ala Ala Thr Gly Gly Leu Thr Ala Asp Glu Ile
355 360 365

Gln Glu Arg Gly Arg Ile Ala Arg Glu Leu Ala Lys Lys Ala Ser Glu
370 375 380

Ala Ala Ala Leu Ala Gln Glu Gly Ser Lys Asn Glu Asp Glu Phe Ala
385 390 395 400

Ile Lys Pro Lys Lys Asp Pro Phe Glu Trp Glu Phe Glu Glu Asp Asp
405 410 415

Phe Glu Asn Glu Glu Asp Glu Ser Asp Ala Asn Ala Val Glu Glu Ser
420 425 430

Thr Glu Thr Ile Val Gly Phe Thr Arg Ile Tyr Ser Gly Ser Leu Ser
435 440 445

Arg Gly Gln Lys Leu Thr Val Ile Gly Pro Lys Tyr Asp Pro Ser Leu
450 455 460

Pro Arg Asp His Gln Thr Asn Phe Glu Gln Ile Thr Asn Glu Val Glu
465 470 475 480

Ile Lys Asp Leu Phe Leu Ile Met Gly Arg Glu Leu Val Arg Met Glu
485 490 495

Lys

<210> 69
<211> 467

<212> PRT
<213> Candida albicans

<400> 69
Pro Ala Gly Asn Ile Val Gly Val Val Gly Leu Asp Asn Ala Val Leu
1 5 10 15

Lys Asn Ala Thr Ile Cys Ser Pro Leu Pro Glu Asp Lys Pro Tyr Ile
20 25 30

Asn Leu Ala Ser Thr Ser Thr Leu Ile His Asn Lys Pro Ile Met Lys
35 40 45

Ile Ala Val Glu Pro Thr Asn Pro Ile Lys Leu Ala Lys Leu Glu Arg
50 55 60

Gly Leu Asp Leu Leu Ala Lys Ala Asp Pro Val Leu Glu Trp Tyr Val
65 70 75 80

Asp Asp Glu Ser Gly Glu Leu Ile Val Cys Val Ala Gly Glu Leu His
85 90 95

Leu Glu Arg Cys Leu Lys Asp Leu Glu Glu Arg Phe Ala Lys Gly Cys
100 105 110

Glu Val Thr Val Lys Glu Pro Val Ile Pro Phe Arg Glu Gly Leu Ala
115 120 125

Asp Asp Lys Ile Ser Thr Asn Thr Asn Asn Asn Asn Asp Asp Asn Glu
130 135 140

Asp His Glu Leu Asp Glu Asn Glu Asp Glu Leu Ala Asp Leu Glu Phe
145 150 155 160

Asp Ile Ser Pro Leu Pro Leu Glu Val Thr Gln Phe Leu Ile Glu Asn
165 170 175

Glu Thr Ile Ile Ala Glu Ile Val Asn Asn Lys Gln Asp Thr His Glu
180 185 190

Ile Arg Asn Asp Phe Ile Glu Lys Phe Ala Thr Ile Ile Asp Asn Ser
195 200 205

Asn Leu Ala Thr Gln Phe Pro Asp Thr Lys Ser Phe Ile Asn Asn Ile
210 215 220

Ile Cys Phe Gly Pro Lys Arg Val Gly Pro Asn Ile Phe Ile Glu Asp
225 230 235 240

Tyr Gly Leu Asn Lys Phe Arg His Leu Leu Gly Glu Ser Ala Thr Glu
245 250 255

Ser Arg Phe Val Tyr Glu Asn Asn Val Phe Asn Gly Val Gln Leu Val
260 265 270

Phe Asn Gly Gly Pro Leu Ala Ser Glu Pro Met Gln Gly Ile Ile Val
275 280 285

Arg Leu Lys Lys Ala Glu Lys Arg Glu Val Asp Glu Asp Lys Ile Val
290 295 300

Asn Pro Gly Lys Ile Ile Thr Gln Thr Arg Asp Leu Ile Tyr Lys Arg
305 310 315 320

Phe Leu Gln Lys Ser Pro Arg Leu Tyr Leu Ala Met Tyr Thr Cys Glu
325 330 335

Ile Gln Ala Ala Ala Glu Val Leu Gly Lys Val Tyr Ala Val Val Gln
340 345 350

Arg Arg Glu Gly Ser Ile Ile Ser Glu Glu Met Lys Glu Gly Thr Pro
355 360 365

Phe Phe Thr Ile Val Ala Arg Ile Pro Val Ile Glu Ala Phe Gly Phe
370 375 380

Ser Glu Asp Ile Arg Lys Lys Thr Ser Gly Ala Ala Ser Pro Gln Leu
385 390 395 400

Val Phe Asp Gly Tyr Asp Met Leu Asp Ile Asp Pro Phe Trp Val Pro
405 410 415

His Thr Glu Glu Glu Leu Glu Glu Leu Gly Glu Phe Ala Glu Arg Glu
420 425 430

Asn Val Ala Arg Arg Tyr Met Asn Asn Ile Arg Arg Arg Lys Gly Leu
435 440 445

Phe Val Asp Glu Lys Val Val Lys Asn Ala Glu Lys Gln Arg Thr Leu
450 455 460

Lys Arg Asp
465

<210> 70

<211> 1340
<212> DNA
<213> Candida albicans

<400> 70
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ttattatgtg atgatatcga tgtttgtgcc aggtgtcaag gtggtaacaa tgctggccac 120
acgattgttg ttggtaaagt caagtatgac ttccacatgt taccttctgg tttggtcaat 180
cctaaatgtc aaaacttagt tggatctggt gttgttatcc acgttccttc cttctttgct 240
gaattggaaa acttggaagc aaaagggtta gattgtcgtg atagattgtt tgtttcatct 300
agagctcatt tggtctttga cttccatcaa cgtactgata aattgaaaga agctgaatta 360
tcaaccaata agaaatcaat aggtactacc ggtaaaggta ttggtccaac ttactcaacc 420
aaggcaagta gatcaggtat cagagtccac catttagtca accctgatcc agaagcttgg 480
gaagaattca aaactagata tttgagatta gtcgagagta gacaaaaaag atacggtgaa 540
tttgaatatg atcctaagga agaattggca agatttgaaa aataccgtga aaccttgaga 600
ccattcgtcg tcgactccgt caacttcatg cacgaagcta ttgctgccaa taaaaaaatc 660
ttggttgaag gtgctaatgc gttaatgttg gatattgatt tcggtactta tccatacgtc 720
acttcttcat caactggtat tggtggtgtt ttgactgggt tgggtattcc tccaagaacc 780
atcagaaatg tctatggtgt tgttaaagcc tacaccacta gagttggtga gggtccattc 840
ccaacagaac aattgaacaa ggtaggtgaa actttgcaag atgttggtgc cgaatatggt 900
gttactactg gaagaaaaag aagatgtggt tggttggatt tggttgtgtt gaaatattcc 960
aacctgatca acggatacac ttctttgaac atcaccaaat tggatgtttt ggataaattc 1020
aaggaaattg aagttggtgt tgcttataaa ttgaatggaa aagagttgcc aagtttccct 1080
gaagatttga ttgatttagc taaagtcgag gttgtgtata agaaattccc aggttgggaa 1140
caagatatca ccggtatcaa gaaatatgaa gacttgccag aaaacgctaa gaactatctt 1200
aaattcattg aagattactt gcaagttcca atccaatggg taggtaccgg tccagctaga 1260
gattctatgt tagaaaagaa gatttagttg tacacatgct acggaagacg attagatttg 1320
ttttattaga ttaataacct 1340

<210> 71
<211> 428
<212> PRT
<213> Candida albicans

<400> 71
Met Cys Asp Val Val Leu Gly Ser Gln Trp Gly Asp Glu Gly Lys Gly
1 5 10 15

Lys Leu Val Asp Leu Leu Cys Asp Asp Ile Asp Val Cys Ala Arg Cys
20 25 30

Gln Gly Gly Asn Asn Ala Gly His Thr Ile Val Val Gly Lys Val Lys
35 40 45

Tyr Asp Phe His Met Leu Pro Ser Gly Leu Val Asn Pro Lys Cys Gln
50 55 60

Asn Leu Val Gly Ser Gly Val Val Ile His Val Pro Ser Phe Phe Ala

65 70 75 80

Glu Leu Glu Asn Leu Glu Ala Lys Gly Leu Asp Cys Arg Asp Arg Leu
85 90 95

Phe Val Ser Ser Arg Ala His Leu Val Phe Asp Phe His Gln Arg Thr
100 105 110

Asp Lys Leu Lys Glu Ala Glu Leu Ser Thr Asn Lys Lys Ser Ile Gly
115 120 125

Thr Thr Gly Lys Gly Ile Gly Pro Thr Tyr Ser Thr Lys Ala Ser Arg
130 135 140

Ser Gly Ile Arg Val His His Leu Val Asn Pro Asp Pro Glu Ala Trp
145 150 155 160

Glu Glu Phe Lys Thr Arg Tyr Leu Arg Leu Val Glu Ser Arg Gln Lys
165 170 175

Arg Tyr Gly Glu Phe Glu Tyr Asp Pro Lys Glu Glu Leu Ala Arg Phe
180 185 190

Glu Lys Tyr Arg Glu Thr Leu Arg Pro Phe Val Val Asp Ser Val Asn
195 200 205

Phe Met His Glu Ala Ile Ala Ala Asn Lys Lys Ile Leu Val Glu Gly
210 215 220

Ala Asn Ala Leu Met Leu Asp Ile Asp Phe Gly Thr Tyr Pro Tyr Val
225 230 235 240

Thr Ser Ser Ser Thr Gly Ile Gly Gly Val Leu Thr Gly Leu Gly Ile
245 250 255

Pro Pro Arg Thr Ile Arg Asn Val Tyr Gly Val Val Lys Ala Tyr Thr
260 265 270

Thr Arg Val Gly Glu Gly Pro Phe Pro Thr Glu Gln Leu Asn Lys Val
275 280 285

Gly Glu Thr Leu Gln Asp Val Gly Ala Glu Tyr Gly Val Thr Thr Gly
290 295 300

Arg Lys Arg Arg Cys Gly Trp Leu Asp Leu Val Val Leu Lys Tyr Ser
305 310 315 320

Asn Ser Ile Asn Gly Tyr Thr Ser Leu Asn Ile Thr Lys Leu Asp Val

325 330 335

Leu Asp Lys Phe Lys Glu Ile Glu Val Gly Val Ala Tyr Lys Leu Asn
340 345 350

Gly Lys Glu Leu Pro Ser Phe Pro Glu Asp Leu Ile Asp Leu Ala Lys
355 360 365

Val Glu Val Val Tyr Lys Lys Phe Pro Gly Trp Glu Gln Asp Ile Thr
370 375 380

Gly Ile Lys Lys Tyr Glu Asp Leu Pro Glu Asn Ala Lys Asn Tyr Leu
385 390 395 400

Lys Phe Ile Glu Asp Tyr Leu Gln Val Pro Ile Gln Trp Val Gly Thr
405 410 415

Gly Pro Ala Arg Asp Ser Met Leu Glu Lys Lys Ile
420 425

<210> 72
<211> 1947
<212> DNA
<213> Candida albicans

<400> 72
atggcttttg atactactgt tcctcaagaa tattatgatg aaaatttttat tcctggtact 60
accaatattt taactggtaa aaccaccatt gatgaatcat catcaataac tactcaaaaa 120
tcattaaaac gagatcccaa aactggatta gtgttaatgc ctcaaccgac atcatcacct 180
aatgatccat taaattggtc tccatttcgt aaatttgctc aattgacatt attatcattt 240
ataacggcat taacggcagc aacttcaaat gatgctggtg ctactcaaga ttcattgaat 300
aaaatatatg gtatttctta tgattcaatg aatactggtg ctggggtatt atttatattt 360
attggatggt catgtatgtt tttcgcacca gcttcttcat tatatggacg aagaataact 420
tatattattt gtttattggc aggaacttta ggttgtgtat ggtttgctct ttctaaaaga 480
actgccgata ctatttggtc acaagcattt gtggggatga gtgaagcttg tgctgaagct 540
caagttcaac aatcattaac tgatttattt ttggctcatg aattgggtac agcattaaca 600
atttatattt ctgctacttc aataggtact ttattgggtc ctttgattgc tcaagatatt 660
gctcaagctc aaactttccg gtgggtcggt tggtggggtg ccattatatg tggtgccact 720
ttgatagtaa tcattttcgg ttgtgaagaa acagtatttg atcgtcaatt atataccaaa 780
gtattagaat ctgaaaatgt tactcaaatt ccagacccat cagaagaaaa gaaacaagat 840
aacccactta caaataatat cattcctcac gagaagaaaa attcaatgga acaagaatta 900
tctcatgaat atatcactgc aaacaataat gaacatgacg ttgttccaat tgatcctgaa 960
actttaaatg aaaagaaaaa atcttattgg caaagaatag caatcattac accagcacct 1020
tatttacaag gtttaggatt taaacaatat ttagaacgtt tcattattta tttcaaaatt 1080
ttcacattac cagcagtttg gttttccgga ttattatggg ggttacaaga tacttatatg 1140
acatttttt taactactca agacacgtat ttttataatc caccatggaa taaatcaaat 1200
gctggtgtag caattatgaa tgtagctaca ttaattggtg ctgttattgg atgcattgtt 1260

tctgggttat tttctgatta tcatgttatt tggttagcta aacggaataa tgggataatg 1320
gaagctgaat atcgattata tttattagtt atcactttaa tcatttcacc cgtagggtta 1380
attatgtttg gtgttggtgc cgctagagaa tggccatggc aagtgattta tgttggatta 1440
ggtttcattg ggtttggttg gggatcaatt ggtgatactt caatgtctta tttaatggat 1500
gcttatcctg atattgtcat tcaaggaatg gtgggagtaa gtattattaa taatactttg 1560
gcttgtattt tcacttttgc ttgttcttat tggttagatg gatcaggaac acaaaacaca 1620
tatattgcct tgtcaattat tgattttgct accatagcat tggttttccc ctttttatat 1680
tatggtaaaa catttagaag gaaaactaaa agactttatg tttcaatggt tgaattgact 1740
caagggatgg gataagagag tgagtggtaa aagaatttta ttaatgatac atttattatt 1800
agaattacta ctatggaaat ccgagtctgt gtttttttta gaagtatatt ttagacgtat 1860
ttagagttgt ttttctcctt tgtactttat ttagcatttt ataatatatt aattcaagtt 1920
gcattaatat atataaataa aaaaact 1947

<210> 73
<211> 584
<212> PRT
<213> Candida albicans

<400> 73

Met Ala Phe Asp Thr Thr Val Pro Gln Glu Tyr Tyr Asp Glu Asn Phe
1 5 10 15

Ile Pro Gly Thr Thr Asn Ile Leu Thr Gly Lys Thr Thr Ile Asp Glu
20 25 30

Ser Ser Ser Ile Thr Thr Gln Lys Ser Leu Lys Arg Asp Pro Lys Thr
35 40 45

Gly Leu Val Leu Met Pro Gln Pro Thr Ser Ser Pro Asn Asp Pro Leu
50 55 60

Asn Trp Ser Pro Phe Arg Lys Phe Ala Gln Leu Thr Leu Leu Ser Phe
65 70 75 80

Ile Thr Ala Leu Thr Ala Ala Thr Ser Asn Asp Ala Gly Ala Thr Gln
85 90 95

Asp Ser Leu Asn Lys Ile Tyr Gly Ile Ser Tyr Asp Ser Met Asn Thr
100 105 110

Gly Ala Gly Val Leu Phe Ile Phe Ile Gly Trp Ser Cys Met Phe Phe
115 120 125

Ala Pro Ala Ser Ser Leu Tyr Gly Arg Arg Ile Thr Tyr Ile Ile Cys
130 135 140

Leu Leu Ala Gly Thr Leu Gly Cys Val Trp Phe Ala Leu Ser Lys Arg
145 150 155 160

Thr Ala Asp Thr Ile Trp Ser Gln Ala Phe Val Gly Met Ser Glu Ala
165 170 175

Cys Ala Glu Ala Gln Val Gln Gln Ser Leu Thr Asp Leu Phe Leu Ala
180 185 190

His Glu Leu Gly Thr Ala Leu Thr Ile Tyr Ile Ser Ala Thr Ser Ile
195 200 205

Gly Thr Leu Leu Gly Pro Leu Ile Ala Gln Asp Ile Ala Gln Ala Gln
210 215 220

Thr Phe Arg Trp Val Gly Trp Trp Gly Ala Ile Ile Cys Gly Ala Thr
225 230 235 240

Leu Ile Val Ile Ile Phe Gly Cys Glu Glu Thr Val Phe Asp Arg Gln
245 250 255

Leu Tyr Thr Lys Val Leu Glu Ser Glu Asn Val Thr Gln Ile Pro Asp
260 265 270

Pro Ser Glu Glu Lys Lys Gln Asp Asn Pro Leu Thr Asn Asn Ile Ile
275 280 285

Pro His Glu Lys Lys Asn Ser Met Glu Gln Glu Leu Ser His Glu Tyr
290 295 300

Ile Thr Ala Asn Asn Asn Glu His Asp Val Val Pro Ile Asp Pro Glu
305 310 315 320

Thr Leu Asn Glu Lys Lys Lys Ser Tyr Trp Gln Arg Ile Ala Ile Ile
325 330 335

Thr Pro Ala Pro Tyr Leu Gln Gly Leu Gly Phe Lys Gln Tyr Leu Glu
340 345 350

Arg Phe Ile Ile Tyr Phe Lys Ile Phe Thr Leu Pro Ala Val Trp Phe
355 360 365

Ser Gly Leu Leu Trp Gly Leu Gln Asp Thr Tyr Met Thr Phe Phe Leu
370 375 380

Thr Thr Gln Asp Thr Tyr Phe Tyr Asn Pro Pro Trp Asn Lys Ser Asn
385 390 395 400

Ala Gly Val Ala Ile Met Asn Val Ala Thr Leu Ile Gly Ala Val Ile
405 410 415

Gly Cys Ile Val Ser Gly Leu Phe Ser Asp Tyr His Val Ile Trp L u
420 425 430

Ala Lys Arg Asn Asn Gly Ile Met Glu Ala Glu Tyr Arg Leu Tyr Leu
435 440 445

Leu Val Ile Thr Leu Ile Ile Ser Pro Val Gly Leu Ile Met Phe Gly
450 455 460

Val Gly Ala Ala Arg Glu Trp Pro Trp Gln Val Ile Tyr Val Gly Leu
465 470 475 480

ggtacgattt ttggtgtgta caagttgcaa gaggggtcta ctggtggcat cagcgatgtc 480
ttgcgtcctg gtaaggagat ggtcgctgcg gggtacacca tgtacggtgc atctgcccat 540
ttggcattga ctacaggtca cggtgtcaat ctttttactt tggatactca gttgggtgaa 600
tttatcttga cccatccaaa cttgaagttg ccagatacta agaacatcta ctcgttgaat 660
gaagggtact cgaacaaatt cccagaatac gttcaagatt atctgaagga cattaaaaag 720
gaagggtaca gtttgagata cattggactg atggttgctg atgtccatcg tactcttttg 780
tatggtggta tttttgctta ccctacatta aagttgagag tgttgtatga atgtttcccc 840
atggccttgt tgatggaaca agcaggcggt tctgctgtca ccatcaaggg tgagaggatc 900
ttggatatct tgccaaaagg tatacacgac aagagttcta ttgtgttggg atccaagggt 960
gaagttgaaa agtatttaaa gcatgtacca aaatagatta tgtagaaaat ttatgaac 1018

<210> 75
<211> 331
<212> PRT
<213> Candida albicans

<400> 75
Met Ser Gly Pro Val Asn Ser Val Ser Lys Gln Met Asn Val Asp Thr
1 5 10 15

Asp Ile Ile Thr Leu Thr Arg Phe Ile Leu Gln Glu Gln Gln Thr Val
20 25 30

Ala Pro Thr Ala Thr Gly Glu Leu Ser Leu Leu Leu Asn Ala Leu Gln
35 40 45

Phe Ala Phe Lys Phe Ile Ala His Asn Ile Arg Arg Ala Glu Leu Val
50 55 60

Asn Leu Ile Gly Val Ser Gly Ser Ala Asn Ser Thr Gly Asp Val Gln
65 70 75 80

Lys Lys Leu Asp Val Ile Gly Asp Glu Ile Phe Ile Asn Ala Met Arg
85 90 95

Ser Ser Asn Asn Val Lys Val Leu Val Ser Glu Glu Gln Glu Asp Leu
100 105 110

Ile Val Phe Pro Gly Gly Gly Thr Tyr Ala Val Cys Thr Asp Pro Ile
115 120 125

Asp Gly Ser Ser Asn Ile Asp Ala Gly Val Ser Val Gly Thr Ile Phe
130 135 140

Gly Val Tyr Lys Leu Gln Glu Gly Ser Thr Gly Gly Ile Ser Asp Val
145 150 155 160

Leu Arg Pro Gly Lys Glu Met Val Ala Ala Gly Tyr Thr Met Tyr Gly

165 170 175

Ala Ser Ala His Leu Ala Leu Thr Thr Gly His Gly Val Asn Leu Phe
180 185 190

Thr Leu Asp Thr Gln Leu Gly Glu Phe Ile Leu Thr His Pro Asn Leu
195 200 205

Lys Leu Pro Asp Thr Lys Asn Ile Tyr Ser Leu Asn Glu Gly Tyr Ser
210 215 220

Asn Lys Phe Pro Glu Tyr Val Gln Asp Tyr Ser Lys Asp Ile Lys Lys
225 230 235 240

Glu Gly Tyr Ser Leu Arg Tyr Ile Gly Ser Met Val Ala Asp Val His
245 250 255

Arg Thr Leu Leu Tyr Gly Gly Ile Phe Ala Tyr Pro Thr Leu Lys Leu
260 265 270

Arg Val Leu Tyr Glu Cys Phe Pro Met Ala Leu Leu Met Glu Gln Ala
275 280 285

Gly Gly Ser Ala Val Thr Ile Lys Gly Glu Arg Ile Leu Asp Ile Leu
290 295 300

Pro Lys Gly Ile His Asp Lys Ser Ser Ile Val Leu Gly Ser Lys Gly
305 310 315 320

Glu Val Glu Lys Tyr Leu Lys His Val Pro Lys
325 330

<210> 76
<211> 1686
<212> DNA
<213> Candida albicans

<400> 76
aattacaatc tggtttgtta ctaccatatc ccattagtgt tattgtcatt gtagatattg 60
ataatggtta aaggattggt tttcattttt tgtgtaatga atgagccaaa ataaaaaatc 120
aattcgatgc gatgcaatga agtttaataa aatttttttt tttctttatt tcttttaatc 180
aacccatcaa tcattaaatt gaatcaatac ctaccattaa catacttcta tatacatata 240
tatatataac aaaatatcat ggggaagata acaactagtg atactaaaac aaaacaacgt 300
cataatccat tattaaaaga tatttcatcc caaggtggga atttaagaac cgttccaaga 360
tcatcatcat catcatcatc acaaaagaag aaatcatcaa agaaacaaag acataacgat 420
gaagacgacg aagaaaatgg tggcggtgaa ggatttttag atgcttctag ttcaagaaag 480
attttacaat tggcaaaaga acaacaagat gaacttgaac aagaagatga aatacaaaat 540

aaaccttcat ttgctcaatc atttaaaaat caacaaatag atagtgaaga agaagaagag 600
gaagatgagt attcagattt tgaagaagaa gaagaagttg aagagatagt atatgatgaa 660
gaagatgcag aagttgatcc caaagatgca gaattattta ataaatattt ccaatccaac 720
ggtgaagcta ataataatga tgatgataat tcatttcaac caacaataaa tttagctgat 780
aaaatcttag ccaaaattca agaaaaagaa tcccaacaac aacaacaaca acaaagctct 840
ccagataata gtaatgaaga tgccgtattg ttaccaccaa aagtcatttt agcttatgaa 900
aaaattggtc aaatttttatc aacttatact catgggaaat tacctaaatt atttaaaatt 960
ttaccaagtt taaaaaattg gcaagatgta ttatacgtga caaatccaaa tagttggact 1020
cctcatgcca catatgaagc aactaaatta tttgtgtcga atttatcaag taatgaagct 1080
acagttttca ttgaaactat cttgttgcca cgattccgtg attctattga aaattccgat 1140
gatcattcat taaattatca tatttatcga gcattaaaaa aatcattata taaaccagga 1200
gctttttca aagggttctt gttaccttta gtcgatggtt attgttctgt acgtgaagcc 1260
actattgctg cttcagtgtt aactaaagtt tctgtccctg ttttacattc atcagttgca 1320
ttaactcaat tattaactag agattttaat cctgctacaa cggttttcat tagagtttta 1380
attgaaaaaa aatatgcttt accttatcaa actttagatg aattagtatt ttatttcatg 1440
agatttagaa atgctactat taatcaagat gaaaatatgg aaaatatgga tattgatcaa 1500
gaaaaaacca ccaaagtcaa taatggtcct caattaccag tggtatggca taaagcattc 1560
ttatcatttg ctactcgtta taaaaatgat cttactgatg atcaaaaaga tttcttatta 1620
gaaacagtaa gacaaagatt tcatcctcta attggtcctg aaattcgtag agaattacta 1680
agttag 1686

<210> 77
<211> 475
<212> PRT
<213> Candida albicans

<400> 77
Met Gly Lys Ile Thr Thr Ser Asp Thr Lys Thr Lys Gln Arg His Asn
1 5 10 15

Pro Leu Leu Lys Asp Ile Ser Ser Gln Gly Gly Asn Leu Arg Thr Val
20 25 30

Pro Arg Ser Ser Ser Ser Ser Ser Ser Gln Lys Lys Lys Ser Ser Lys
35 40 45

Lys Gln Arg His Asn Asp Glu Asp Asp Glu Glu Asn Gly Gly Gly Glu
50 55 60

Gly Phe Leu Asp Ala Ser Ser Ser Arg Lys Ile Leu Gln Leu Ala Lys
65 70 75 80

Glu Gln Gln Asp Glu Leu Glu Gln Glu Asp Glu Ile Gln Asn Lys Pro
85 90 95

Ser Phe Ala Gln Ser Phe Lys Asn Gln Gln Ile Asp Ser Glu Glu Glu
100 105 110

Glu Glu Glu Asp Glu Tyr Ser Asp Phe Glu Glu Glu Glu Glu Val Glu
115 120 125

Glu Ile Val Tyr Asp Glu Glu Asp Ala Glu Val Asp Pro Lys Asp Ala
130 135 140

Glu Leu Phe Asn Lys Tyr Phe Gln Ser Asn Gly Glu Ala Asn Asn Asn
145 150 155 160

Asp Asp Asp Asn Ser Phe Gln Pro Thr Ile Asn Leu Ala Asp Lys Ile
165 170 175

Leu Ala Lys Ile Gln Glu Lys Glu Ser Gln Gln Gln Gln Gln Gln Gln
180 185 190

Ser Ser Pro Asp Asn Ser Asn Glu Asp Ala Val Leu Leu Pro Pro Lys
195 200 205

Val Ile Leu Ala Tyr Glu Lys Ile Gly Gln Ile Leu Ser Thr Tyr Thr
210 215 220

His Gly Lys Leu Pro Lys Leu Phe Lys Ile Leu Pro Ser Leu Lys Asn
225 230 235 240

Trp Gln Asp Val Leu Tyr Val Thr Asn Pro Asn Ser Trp Thr Pro His
245 250 255

Ala Thr Tyr Glu Ala Thr Lys Leu Phe Val Ser Asn Leu Ser Ser Asn
260 265 270

Glu Ala Thr Val Phe Ile Glu Thr Ile Leu Leu Pro Arg Phe Arg Asp
275 280 285

Ser Ile Glu Asn Ser Asp Asp His Ser Leu Asn Tyr His Ile Tyr Arg
290 295 300

Ala Leu Lys Lys Ser Leu Tyr Lys Pro Gly Ala Phe Phe Lys Gly Phe
305 310 315 320

Leu Leu Pro Leu Val Asp Gly Tyr Cys Ser Val Arg Glu Ala Thr Ile
325 330 335

Ala Ala Ser Val Leu Thr Lys Val Ser Val Pro Val Leu His Ser Ser
340 345 350

Val Ala Leu Thr Gln Leu Leu Thr Arg Asp Phe Asn Pro Ala Thr Thr
355 360 365

Val Phe Ile Arg Val Leu Ile Glu Lys Lys Tyr Ala Leu Pro Tyr Gln
370 375 380

Thr Leu Asp Glu Leu Val Phe Tyr Phe Met Arg Phe Arg Asn Ala Thr
385 390 395 400

Ile Asn Gln Asp Glu Asn Met Glu Asn Met Asp Ile Asp Gln Glu Lys
405 410 415

Thr Thr Lys Val Asn Asn Gly Pro Gln Leu Pro Val Val Trp His Lys
420 425 430

Ala Phe Leu Ser Phe Ala Thr Arg Tyr Lys Asn Asp Leu Thr Asp Asp
435 440 445

Gln Lys Asp Phe Leu Leu Glu Thr Val Arg Gln Arg Phe His Pro Leu
450 455 460

Ile Gly Pro Glu Ile Arg Arg Glu Leu Leu Ser
465 470 475

<210> 78
<211> 1519
<212> DNA
<213> Candida albicans

<400> 78
accatgtgtc aaattgcttg gtcgtgtcct ttcaccacac atttttttgg attaaatttc 60
tcgcacgctc aaaaaatgac ttcgacaaaa agcaatgcca ctcttcctac aattaattcc 120
ctccgccccc tccttttcat atactatctc ccttccttct tccttctcct tttatttttt 180
caattattac aatcttatgt catttaaagg attcaaaaag ggtgtcctta gggccccaca 240
gacaatgcgt cagaaattca acatgggaga aatcacccaa gatgctgttt atcttcgatgc 300
tgaaagaaga ttcaaagaaa tcgaaacgga aacaaaaaag ttgagtgaag aatccaagaa 360
atatttcaat gctgtcaatg ggatgttaga tgaacaaatt gattttgcca aagccgtggc 420
tgagatttat aaaccaatca gtggtagatt atcggacccc agtgctacgg taccagaaga 480
taacccacaa ggtattgaag catcggaact gtaccaagca gtggttaaag atcttcaaaga 540
taccttaaaa cccgatttgg aattgattga aaaaagaatt gttgaaccag cacaagaatt 600
attgaagatt atacaagcta taaggaaaat gtcagtgaaa agagaccata aacaattgga 660
tttggatcgt cataagagaa atttttctaa atatgaactg aagaaagaaa gaactgttaa 720
agatgaagaa aaaatgttca gtgctcaagc agaagtagaa attgctcaac aagagtacga 780
ttattataat gatttgttaa agaatgaatt gccagttttg tttcaaatgc aaagtgattt 840
tatcaaacca ttgtttgttt cattctatta catgcagttg aatattttct acacattata 900
cactagaatg gaagagttga aaattccata ttttgatttg tctactgata ttgtcgaagc 960
ttatactgcc aagaagggga acattgagga acaaaccgat gctattggaa tcactcattt 1020
caaagtcggg catgccaaat ccaaattgga agccactaaa agaagacatg ctgctatgaa 1080
tagtccacct cctaccggtg ccagctctat tgcatctaca ggtactggtg gtgaattacc 1140
tgcatactcc ccaggaggtt acaaccaacc atatggtgat agcaagtatc aaccaccatc 1200

ttctccagca acataccaat ctccagtagt agcagccact gctcaatctc cagctactta 1260
tcaatcgcca gtggctactg gacaacctcc atcatattta ccacaaactc cagccagtgc 1320
tccaccacca caagttggta gtggccttcc aacatgcacg gctttatacg attatactgc 1380
acaagcccag ggtgacttga ctttccctgc aggagctgtt attgaaatta tacaaagaac 1440
cgaagatgcc aacggatggt ggactggtaa atacaatggt caaaccggtg tgttccctgg 1500
taattatgtg caattatag 1519

<210> 79
<211> 440
<212> PRT
<213> Candida albicans

<400> 79

Met Ser Phe Lys Gly Phe Lys Lys Gly Val Leu Arg Ala Pro Gln Thr
1 5 10 15

Met Arg Gln Lys Phe Asn Met Gly Glu Ile Thr Gln Asp Ala Val Tyr
20 25 30

Leu Asp Ala Glu Arg Arg Phe Lys Glu Ile Glu Thr Glu Thr Lys Lys
35 40 45

Leu Ser Glu Glu Ser Lys Lys Tyr Phe Asn Ala Val Asn Gly Met Leu
50 55 60

Asp Glu Gln Ile Asp Phe Ala Lys Ala Val Ala Glu Ile Tyr Lys Pro
65 70 75 80

Ile Ser Gly Arg Leu Ser Asp Pro Ser Ala Thr Val Pro Glu Asp Asn
85 90 95

Pro Gln Gly Ile Glu Ala Ser Glu Ser Tyr Gln Ala Val Val Lys Asp
100 105 110

Leu Lys Asp Thr Leu Lys Pro Asp Leu Glu Leu Ile Glu Lys Arg Ile
115 120 125

Val Glu Pro Ala Gln Glu Leu Leu Lys Ile Ile Gln Ala Ile Arg Lys
130 135 140

Met Ser Val Lys Arg Asp His Lys Gln Leu Asp Leu Asp Arg His Lys
145 150 155 160

Arg Asn Phe Ser Lys Tyr Glu Ser Lys Lys Glu Arg Thr Val Lys Asp
165 170 175

Glu Glu Lys Met Phe Ser Ala Gln Ala Glu Val Glu Ile Ala Gln Gln
180 185 190

Glu Tyr Asp Tyr Tyr Asn Asp Leu Leu Lys Asn Glu Leu Pro Val Leu
195 200 205

Phe Gln Met Gln Ser Asp Phe Ile Lys Pro Leu Phe Val Ser Phe Tyr
210 215 220

Tyr Met Gln Leu Asn Ile Phe Tyr Thr Leu Tyr Thr Arg Met Glu Glu
225 230 235 240

Leu Lys Ile Pro Tyr Phe Asp Leu Ser Thr Asp Ile Val Glu Ala Tyr
245 250 255

Thr Ala Lys Lys Gly Asn Ile Glu Glu Gln Thr Asp Ala Ile Gly Ile
260 265 270

Thr His Phe Lys Val Gly His Ala Lys Ser Lys Leu Glu Ala Thr Lys
275 280 285

Arg Arg His Ala Ala Met Asn Ser Pro Pro Pro Thr Gly Ala Ser Ser
290 295 300

Ile Ala Ser Thr Gly Thr Gly Gly Glu Leu Pro Ala Tyr Ser Pro Gly
305 310 315 320

Gly Tyr Asn Gln Pro Tyr Gly Asp Ser Lys Tyr Gln Pro Pro Ser Ser
325 330 335

Pro Ala Thr Tyr Gln Ser Pro Val Val Ala Ala Thr Ala Gln Ser Pro
340 345 350

Ala Thr Tyr Gln Ser Pro Val Ala Thr Gly Gln Pro Pro Ser Tyr Leu
355 360 365

Pro Gln Thr Pro Ala Ser Ala Pro Pro Pro Gln Val Gly Ser Gly Leu
370 375 380

Pro Thr Cys Thr Ala Leu Tyr Asp Tyr Thr Ala Gln Ala Gln Gly Asp
385 390 395 400

Leu Thr Phe Pro Ala Gly Ala Val Ile Glu Ile Ile Gln Arg Thr Glu
405 410 415

Asp Ala Asn Gly Trp Trp Thr Gly Lys Tyr Asn Gly Gln Thr Gly Val
420 425 430

Phe Pro Gly Asn Tyr Val Gln Leu
435 440

<210> 80
<211> 861
<212> DNA
<213> Candida albicans

<400> 80
atgtctataa ttttcagaaa gagactagat tctgatagaa atatagacgc atcactatat 60
tttggaaata tagatccaca agttacggag ttgttaatgt atgagttgtt catccaattt 120
ggtcccgtca aatcaatcaa tatgccaaag gatcgtatat tgaaaacaca ccaggggtat 180
ggatttgtcg aatttaaaaa ctcagcagat gccaaatata ctatggaaat actacgagga 240
ataagacttt atggaaaagc attgaaattg aaacgaattg atgccaagtc tcagtcatca 300
acaaacaacc caaataatca aacaatagga acatttgtac aatcagattt gatcaatcca 360
aattacatag atgttggagc taaactattt atcaacaatc ttaatccatt ggtcgatgaa 420
tccttttaa tggatacgtt tagtaagttt ggaaccctta taagaaaccc aataattaga 480
cgtgattcag agggacactc tttgggatac ggatttctta cgtacgatga ctttgaaagt 540
agtgatttat gcatacaaaa aatgaacaac acgattttga tgaataacaa aattgctatc 600
agttatgcat tcaaggatct gagtgttgat gggaagaaat cccggcatgg agatcaagtg 660
gagcggaaat tggctgaaag tgccaaaaag aataatttgt tggtaacgaa aacttctaag 720
gcaggtacga cgaagggaaa taaaaggaag aataaaccac ataaagtgac caaaccgtga 780
gacaatgagt tagctccccc tttcaaaata agtagagtat caccatagtt tatgaaacaa 840
ttgatatatt aagcttctct g 861

<210> 81
<211> 1641
<212> DNA
<213> Candida albicans

<400> 81
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agtgcataca ttggtatcat cattatgtgt ttccttattg cctttggtgg ttttgttttc 180
ggtttcgata ctggtaccat ttctggtttt attaatatgt ctgacttttt agaaagattc 240
ggtggtacta aagctgacgg tactctttac ttttccaatg tcagaactgg tgtaatgatt 300
ggtttgttca acgctggtgg tgccattggt gcattattct tgtctaaagt cggtgatatg 360
tatggtagaa gagttggtat catgactgct atgattgtct atattgttgg tattattgtt 420
caaattgctt ctcaacatgc ttggtatcaa gtcatgattg gtagaattat cactggtctt 480
gccgttggta tgttatcagt tttatgtcct ttgttcattt ccgaggtttc tccaaaacat 540
ttgagaggta ctttggtgtg ctgtttccaa ttgatgatta ccttgggtat cttcttgggt 600
tattgtacta cctatggtac taagagttac tcagactcta gacaatggag aattccattg 660
ggtttatgtt tcgcctgggc tttatgtttg gttgctggta tggttagaat gccagaatct 720
ccacgttacc ttgtcggtaa agacagaatt gaagatgcta aaatgtcact tgccaaaact 780
aacaaggttt ctccagagga cccagcatta taccgtgaac ttcaattaat ccaagctggt 840
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agaatctttg aaagagttat tgttggtgtc atgttacaag ccttacaaca attaactggt 960
gataactatt tcttctacta cagtaccacc attttcaagt ccgttggtat gaatgattcc 1020
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gctattgaaa gaatgggtag aagactctgt ttgttaactg gttccgttgc catgtcaatc 1140
tgtttcttaa tctattcctt ggttggtact caacatcttt atattgacaa accaggtggt 1200
gctagtagaa aaccagatgg tgatgccatg atctttatga ctccacttta tgtgatcttc 1260
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ggatgtttag ttttctccat tttctttgtc tactttatgg tttacgaaac taaaggtctt 1500
accttggaag aaattgatga attgtactcc accaaagtcc ttccatggaa atcagctggt 1560
tgggtgccac cttccgaaga agaaatggca acctctacgg gatatgctgg tgatgccaaa 1620
ccagaagagg aacacgttta a 1641

<210> 82
<211> 546
<212> PRT
<213> Candida albicans

<400> 82
Met Ser Gln Asp Asn Val Ser Ser Thr Ser Thr Ala Glu Ala Val Asn
1 5 10 15

Asn Glu Ile Lys Val Lys Asp Glu Phe Pro Gln Glu Glu Gln Ala His
20 25 30

Thr Ser Leu Glu Asp Lys Pro Val Ser Ala Tyr Ile Gly Ile Ile Ile
35 40 45

Met Cys Phe Leu Ile Ala Phe Gly Gly Phe Val Phe Gly Phe Asp Thr
50 55 60

Gly Thr Ile Ser Gly Phe Ile Asn Met Ser Asp Phe Leu Glu Arg Phe
65 70 75 80

Gly Gly Thr Lys Ala Asp Gly Thr Leu Tyr Phe Ser Asn Val Arg Thr
85 90 95

Gly Val Met Ile Gly Leu Phe Asn Ala Gly Gly Ala Ile Gly Ala Leu
100 105 110

Phe Leu Ser Lys Val Gly Asp Met Tyr Gly Arg Arg Val Gly Ile Met
115 120 125

Thr Ala Met Ile Val Tyr Ile Val Gly Ile Ile Val Gln Ile Ala Ser
130 135 140

Gln His Ala Trp Tyr Gln Val Met Ile Gly Arg Ile Ile Thr Gly Leu
145 150 155 160

Ala Val Gly Met Leu Ser Val Leu Cys Pro Leu Phe Ile Ser Glu Val

165 170 175

Ser Pro Lys His Leu Arg Gly Thr Leu Val Cys Cys Phe Gln Leu Met
180 185 190

Ile Thr Leu Gly Ile Phe Leu Gly Tyr Cys Thr Thr Tyr Gly Thr Lys
195 200 205

Ser Tyr Ser Asp Ser Arg Gln Trp Arg Ile Pro Leu Gly Leu Cys Phe
210 215 220

Ala Trp Ala Leu Cys Leu Val Ala Gly Met Val Arg Met Pro Glu Ser
225 230 235 240

Pro Arg Tyr Leu Val Gly Lys Asp Arg Ile Glu Asp Ala Lys Met Ser
245 250 255

Leu Ala Lys Thr Asn Lys Val Ser Pro Glu Asp Pro Ala Leu Tyr Arg
260 265 270

Glu Leu Gln Leu Ile Gln Ala Gly Val Glu Arg Glu Arg Leu Ala Gly
275 280 285

Lys Ala Ser Trp Gly Thr Leu Phe Asn Gly Lys Pro Arg Ile Phe Glu
290 295 300

Arg Val Ile Val Gly Val Met Leu Gln Ala Leu Gln Gln Leu Thr Gly
305 310 315 320

Asp Asn Tyr Phe Phe Tyr Tyr Ser Thr Thr Ile Phe Lys Ser Val Gly
325 330 335

Met Asn Asp Ser Phe Glu Thr Ser Ile Ile Ile Gly Val Ile Asn Phe
340 345 350

Ala Ser Thr Phe Val Gly Ile Tyr Ala Ile Glu Arg Met Gly Arg Arg
355 360 365

Leu Cys Leu Leu Thr Gly Ser Val Ala Met Ser Ile Cys Phe Leu Ile
370 375 380

Tyr Ser Leu Val Gly Thr Gln His Leu Tyr Ile Asp Lys Pro Gly Gly
385 390 395 400

Ala Ser Arg Lys Pro Asp Gly Asp Ala Met Ile Phe Met Thr Pro Leu
405 410 415

Tyr Val Ile Phe Ser Pro Ser Thr Trp Ala Gly Gly Val Tyr Ser Ile

420 425 430

Ile Ser Glu Leu Tyr Pro Leu Lys Val Arg Ser Lys Ala Met Gly Leu
435 440 445

Ala Asn Ala Ser Asn Trp Thr Trp Gly Phe Leu Ile Ser Phe Phe Thr
450 455 460

Ser Phe Ile Thr Asp Ala Ile His Phe Tyr Tyr Gly Phe Val Phe Met
465 470 475 480

Gly Cys Leu Val Phe Ser Ile Phe Phe Val Tyr Phe Met Val Tyr Glu
485 490 495

Thr Lys Gly Leu Thr Leu Glu Glu Ile Asp Glu Leu Tyr Ser Thr Lys
500 505 510

Val Leu Pro Trp Lys Ser Ala Gly Trp Val Pro Pro Ser Glu Glu Glu
515 520 525

Met Ala Thr Ser Thr Gly Tyr Ala Gly Asp Ala Lys Pro Glu Glu Glu
530 535 540

His Val
545

<210> 83
<211> 1014
<212> DNA
<213> Candida albicans

<400> 83
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gttggccaag aaatcattaa gatggaagaa ggcgacgccc cagccggcgg tgcatctgca 120
tctgaagctc cagctaagaa agaagaagcc cctgaaaagg ctaaagaaga atctgctcaa 180
gctgccgcac caaagaagga agaaactaag aaagaggaac caaagaagga atcaaaacca 240
gctccaaaga aagaagaatc taagaagtcc acccaatcta caactagtgc tccaactttc 300
accaatttct ccagaaacga agagagagtt aagatgaaca gaatgagatt gagaattgct 360
gaacgtctta aggaatcaca aaacactgct gcttccttga ccactttcaa cgaagttgat 420
atgtctaact tgatggattt cagaaagaaa tacaaggacg aatttattga aaagaccggt 480
atcaagttag gattcatggg tgctttctcc aaagcttctg ccttggctct taaggaaatc 540
ccagctgtca atgctgcaat tgaaaacaat gacactttgg tctttaaaga ttatgccgac 600
atttcaattg ctgttgccac tccaaaaggt ttggtgaccc ctgttgtcag aaacgccgaa 660
tccttatcta ttttgggtat tgaaaaggaa atctctaatt tgggtaagaa agccagagat 720
ggtaaattga ctttggaaga tatgaccggt ggtactttca ctatttctaa tggtggtgtt 780
tttggatcat tatacggtac cccaattatc aatatgcctc aaactgccgt attaggttta 840
cacggtgtta aagaaagacc agttactggt aacggtcaaa ttgttttctag accaatgatg 900

tacttagcat tgacttacga ccacagagta gttgacggtc gtgaagctgt tattttctta 960
agaaccatca aggaattgat tgaagatcca agaaagatgt tgttgttaga ataa 1014

<210> 84
<211> 337
<212> PRT
<213> Candida albicans

<400> 84
Asn Ala Pro Val Ser Gly Thr Ile Thr Glu Phe Leu Val Asp Val Asp
1 5 10 15

Ala Thr Val Glu Val Gly Gln Glu Ile Ile Lys Met Glu Glu Gly Asp
20 25 30

Ala Pro Ala Gly Gly Ala Ser Ala Ser Glu Ala Pro Ala Lys Lys Glu
35 40 45

Glu Ala Pro Glu Lys Ala Lys Glu Glu Ser Ala Gln Ala Ala Ala Pro
50 55 60

Lys Lys Glu Glu Thr Lys Lys Glu Glu Pro Lys Lys Glu Ser Lys Pro
65 70 75 80

Ala Pro Lys Lys Glu Glu Ser Lys Lys Ser Thr Gln Ser Thr Thr Ser
85 90 95

Ala Pro Thr Phe Thr Asn Phe Ser Arg Asn Glu Glu Arg Val Lys Met
100 105 110

Asn Arg Met Arg Leu Arg Ile Ala Glu Arg Leu Lys Glu Ser Gln Asn
115 120 125

Thr Ala Ala Ser Leu Thr Thr Phe Asn Glu Val Asp Met Ser Asn Leu
130 135 140

Met Asp Phe Arg Lys Lys Tyr Lys Asp Glu Phe Ile Glu Lys Thr Gly
145 150 155 160

Ile Lys Leu Gly Phe Met Gly Ala Phe Ser Lys Ala Ser Ala Leu Ala
165 170 175

Leu Lys Glu Ile Pro Ala Val Asn Ala Ala Ile Glu Asn Asn Asp Thr
180 185 190

Leu Val Phe Lys Asp Tyr Ala Asp Ile Ser Ile Ala Val Ala Thr Pro
195 200 205

Lys Gly Leu Val Thr Pro Val Val Arg Asn Ala Glu Ser Leu Ser Ile
210 215 220

Leu Gly Ile Glu Lys Glu Ile Ser Asn Leu Gly Lys Lys Ala Arg Asp
225 230 235 240

Gly Lys Leu Thr Leu Glu Asp Met Thr Gly Gly Thr Phe Thr Ile Ser
245 250 255

Asn Gly Gly Val Phe Gly Ser Leu Tyr Gly Thr Pro Ile Ile Asn Met
260 265 270

Pro Gln Thr Ala Val Leu Gly Leu His Gly Val Lys Glu Arg Pro Val
275 280 285

Thr Val Asn Gly Gln Ile Val Ser Arg Pro Met Met Tyr Leu Ala Leu
290 295 300

Thr Tyr Asp His Arg Val Val Asp Gly Arg Glu Ala Val Ile Phe Leu
305 310 315 320

Arg Thr Ile Lys Glu Leu Ile Glu Asp Pro Arg Lys Met Leu Leu Leu
325 330 335

Glu

<210> 85
<211> 1806
<212> DNA
<213> Candida albicans

<400> 85
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caactcctcc taaggttgcc aaatcaaaat cttcgacaat tggtaaaata ttcagataca 180
ctttttacac tgctgtgata tcggttattg gttctgccgg tttgatcggt tacaaaattt 240
acgaagagtc tcaacctgtt gatcaagtga aacaaacacc attgtttcct aatggtgaaa 300
aaaagaaaac tttagttatt ttgggttctg gttggggtgc tatttcatta ttgaaaaact 360
tggataccac cttgtataat gttgttattg tctccccaag aaactatttc cttttcaccc 420
cattgttacc atctgttcct accggtactg ttgaattgag atctattatt gaacctgtca 480
gatcagtcac cagaagatgc cctggtcaag ttatttacct tgaagcagaa gctacaaata 540
tcaaccctaa aactaatgag ttgacactta aacaaagtac tactgtcgtt tctggtcatt 600
ctggtaaaga tacttcctct tctaaatcaa ctgttgccga atacactggg gttgaagaaa 660
tcactaccac cttgaattat gactatttag ttgttggtgt tggtgctcaa ccatctactt 720
tcggtattcc tggagtcgct gagaattcaa ccttttttgaa agaagtcagt gatgcttctg 780
ctattagaag aaaattgatg gatgttattg aagctgccaa tattttacct aaaagctgac 840

cagaaagaaa gagattattg tccattgttg tttgtggagg tggaccaacg ggtgttgaag 900
ctgctggtga aatccaagat tatattgacc aagatttgaa gaaatgggtt cctgaagttg 960
ccgatgaatt gaaagtctcc ttggtggaag ctttaccaaa cgttttgaac acatttaaca 1020
agaaattgat tgactatacc aaagaagttt tcaaagacac taatatcaat ttgatgacta 1080
ataccatgat caaaaaagtc aatgataaaa gtttgattgc aaaccataaa aaccctgacg 1140
gatctactga gtctattgaa attccatatg gtcttttaat ttgggctact ggtaatgcac 1200
caagagattt cactcgtgat ttgatcgcaa aagtcgatga acaaaaaaat gccagaagag 1260
gtttattggt tgatgaaaga ttgaaagttg atggtactga taacattttt gccttgggtg 1320
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tagccaatta ttttgacaaa ttgcatgcgg ttgaatcttt gaaatacacc attgctaacc 1440
caactccaaa ggacaatgtt gaaaaattgt caagaaaatt agctagatta gaaaagaatt 1500
tacctcattt catttacaac taccaagggt ctttggctta cattgggtct gaaaaggctg 1560
ttgctgattt ggtctggggt gattggtcaa atataagttc cggaggtaat ttgacctttt 1620
tattctggag atcagcttat atttacatgt gtttatcagt caagaaccaa gtgctagttg 1680
ttttagattg ggctaaagtc tatttctttg gtagagattg ttctaaggaa tagataccct 1740
gagtttaccc ttacttttt ttgtgattta atttgattag aaaattcatt atttattcat 1800
agccgt 1806

<210> 86
<211> 574
<212> PRT
<213> Candida albicans

<400> 86
Met Phe Thr Arg Ser Leu Ile Lys Gly Gly Gly Arg Leu Ala Thr Thr
1 5 10 15

Arg Ser Leu Val Asn Asn Ser Thr Ser Leu Val Leu Lys Asn Gln Phe
20 25 30

Lys Lys Tyr Ser Thr Ser Thr Pro Pro Lys Val Ala Lys Ser Lys Ser
35 40 45

Ser Thr Ile Gly Lys Ile Phe Arg Tyr Thr Phe Tyr Thr Ala Val Ile
50 55 60

Ser Val Ile Gly Ser Ala Gly Leu Ile Gly Tyr Lys Ile Tyr Glu Glu
65 70 75 80

Ser Gln Pro Val Asp Gln Val Lys Gln Thr Pro Leu Phe Pro Asn Gly
85 90 95

Glu Lys Lys Lys Thr Leu Val Ile Leu Gly Ser Gly Trp Gly Ala Ile
100 105 110

Ser Leu Leu Lys Asn Leu Asp Thr Thr Leu Tyr Asn Val Val Ile Val
115 120 125

Ser Pro Arg Asn Tyr Phe Leu Phe Thr Pro Leu Leu Pro Ser Val Pro
130 135 140

Thr Gly Thr Val Glu Leu Arg Ser Ile Ile Glu Pro Val Arg Ser Val
145 150 155 160

Thr Arg Arg Cys Pro Gly Gln Val Ile Tyr Leu Glu Ala Glu Ala Thr
165 170 175

Asn Ile Asn Pro Lys Thr Asn Glu Leu Thr Leu Lys Gln Ser Thr Thr
180 185 190

Val Val Ser Gly His Ser Gly Lys Asp Thr Ser Ser Ser Lys Ser Thr
195 200 205

Val Ala Glu Tyr Thr Gly Val Glu Glu Ile Thr Thr Thr Leu Asn Tyr
210 215 220

Asp Tyr Leu Val Val Gly Val Gly Ala Gln Pro Ser Thr Phe Gly Ile
225 230 235 240

Pro Gly Val Ala Glu Asn Ser Thr Phe Leu Lys Glu Val Ser Asp Ala
245 250 255

Ser Ala Ile Arg Arg Lys Leu Met Asp Val Ile Glu Ala Ala Asn Ile
260 265 270

Leu Pro Lys Asp Asp Pro Glu Arg Lys Arg Leu Leu Ser Ile Val Val
275 280 285

Cys Gly Gly Gly Pro Thr Gly Val Glu Ala Ala Gly Glu Ile Gln Asp
290 295 300

Tyr Ile Asp Gln Asp Leu Lys Lys Trp Val Pro Glu Val Ala Asp Glu
305 310 315 320

Leu Lys Val Ser Leu Val Glu Ala Leu Pro Asn Val Leu Asn Thr Phe
325 330 335

Asn Lys Lys Leu Ile Asp Tyr Thr Lys Glu Val Phe Lys Asp Thr Asn
340 345 350

Ile Asn Leu Met Thr Asn Thr Met Ile Lys Lys Val Asn Asp Lys Ser
355 360 365

Leu Ile Ala Asn His Lys Asn Pro Asp Gly Ser Thr Glu Ser Ile Glu
370 375 380

Ile Pro Tyr Gly Leu Leu Ile Trp Ala Thr Gly Asn Ala Pro Arg Asp
385 390 395 400

Phe Thr Arg Asp Leu Ile Ala Lys Val Asp Glu Gln Lys Asn Ala Arg
405 410 415

Arg Gly Leu Leu Val Asp Glu Arg Leu Lys Val Asp Gly Thr Asp Asn
420 425 430

Ile Phe Ala Leu Gly Asp Cys Thr Phe Thr Lys Tyr Pro Pro Thr Ala
435 440 445

Gln Val Ala Phe Gln Glu Gly Glu Tyr Leu Ala Asn Tyr Phe Asp Lys
450 455 460

Leu His Ala Val Glu Ser Leu Lys Tyr Thr Ile Ala Asn Pro Thr Pro
465 470 475 480

Lys Asp Asn Val Glu Lys Leu Ser Arg Lys Leu Ala Arg Leu Glu Lys
485 490 495

Asn Leu Pro His Phe Ile Tyr Asn Tyr Gln Gly Ser Leu Ala Tyr Ile
500 505 510

Gly Ser Glu Lys Ala Val Ala Asp Leu Val Trp Gly Asp Trp Ser Asn
515 520 525

Ile Ser Ser Gly Gly Asn Leu Thr Phe Leu Phe Trp Arg Ser Ala Tyr
530 535 540

Ile Tyr Met Cys Leu Ser Val Lys Asn Gln Val Leu Val Val Leu Asp
545 550 555 560

Trp Ala Lys Val Tyr Phe Phe Gly Arg Asp Cys Ser Lys Glu
565 570

<210> 87
<211> 1137
<212> DNA
<213> Candida albicans

<400> 87
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gcagagctag atattttaaa gaggtgctat atatgcaaag atctattgaa tgcacccgtg 120
aggacacaat gtgatcacac gtactgttca caatgtatac gagaattttt acttcgagat 180
aatagatgtc cgctttgtaa aacagaggtt tttgaaagtg gtctaaaacg tgatccattg 240
ttagaagaga tcgtcgttag ttatgcctcc cttaggcctc atttattacg aattgggag 300

attgaaaagg tggaatcgaa gcaagaggta gatcgtgaga aatcagccaa tgagtcagcg 360
ctgaatggta atagaaatgt aaacaacgat gttgacgaaa ctgcgcgcgt taaagatcaa 420
ctgaatgcag atgaactagg tgaagaaaaa gggcaagctc aacatgggga acaagtaaac 480
gagcagacta ctgaagttat tctgttgcta tctgatgatg aagagaatgg ttctgatagc 540
ctagtaaaat gtcctatttg ttttgagaga atggaattag atgtactaca gggaaagcat 600
attgacgact gtctaagtgg aaagagcacg aagaggacgc ctacagacat tttatcccca 660
aaagccaaac gaccgaagca aatcacctcc tttttcaaac caacaataga tactaaaacg 720
ccttcgccac ctacaagtaa ggcgtcaaca actccaacag caactccgac aactacattg 780
ttgaaagcaa acgtcgcatc tccatcccca gtggcgcaaa gtacagttca caagggcaag 840
ccattaccta aactcgattt cagcagcttg agtactcaaa aaattaaagc caagttgagt 900
gatttgaaac tacccacaac aggtagtagg aatgaaatgg aagccagata cttgcattac 960
tacgtgattt ataatgccaa ccttgattcc aatcatcctg taaaggaatc tattttgcga 1020
caacagttga aacaatggga aatggtgcaa catcaaccgt cgtttggtga tgcagagtgg 1080
aaaggagctg aaactgggaa ttggaaagaa ctcattgcaa gagcacggag taactaa 1137

<210> 88
<211> 378
<212> PRT
<213> Candida albicans

<400> 88
Met Asn Leu Lys Asp Ile Thr Asp Pro Ser Asp Phe Lys Thr Thr Lys
1 5 10 15

Leu Pro Ala Leu Ala Glu Leu Asp Ile Leu Lys Arg Cys Tyr Ile Cys
20 25 30

Lys Asp Leu Leu Asn Ala Pro Val Arg Thr Gln Cys Asp His Thr Tyr
35 40 45

Cys Ser Gln Cys Ile Arg Glu Phe Leu Leu Arg Asp Asn Arg Cys Pro
50 55 60

Leu Cys Lys Thr Glu Val Phe Glu Ser Gly Leu Lys Arg Asp Pro Leu
65 70 75 80

Leu Glu Glu Ile Val Val Ser Tyr Ala Ser Leu Arg Pro His Leu Leu
85 90 95

Arg Leu Leu Glu Ile Glu Lys Val Glu Ser Lys Gln Glu Val Asp Arg
100 105 110

Glu Lys Ser Ala Asn Glu Ser Ala Ser Asn Gly Asn Arg Asn Val Asn
115 120 125

Asn Asp Val Asp Glu Thr Ala Arg Val Lys Asp Gln Ser Asn Ala Asp
130 135 140

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Glu Leu Gly Glu Glu Lys Gly Gln Ala Gln His Gly Glu Gln Val Asn
145                 150                 155                 160

Glu Gln Thr Thr Glu Val Ile Ser Leu Leu Ser Asp Asp Glu Glu Asn
                165                 170                 175

Gly Ser Asp Ser Leu Val Lys Cys Pro Ile Cys Phe Glu Arg Met Glu
            180                 185                 190

Leu Asp Val Leu Gln Gly Lys His Ile Asp Asp Cys Leu Ser Gly Lys
        195                 200                 205

Ser Thr Lys Arg Thr Pro Thr Asp Ile Leu Ser Pro Lys Ala Lys Arg
    210                 215                 220

Pro Lys Gln Ile Thr Ser Phe Phe Lys Pro Thr Ile Asp Thr Lys Thr
225                 230                 235                 240

Pro Ser Pro Pro Thr Ser Lys Ala Ser Thr Thr Pro Thr Ala Thr Pro
                245                 250                 255

Thr Thr Thr Leu Leu Lys Ala Asn Val Ala Ser Pro Ser Pro Val Ala
            260                 265                 270

Gln Ser Thr Val His Lys Gly Lys Pro Leu Pro Lys Leu Asp Phe Ser
        275                 280                 285

Ser Leu Ser Thr Gln Lys Ile Lys Ala Lys Leu Ser Asp Leu Lys Leu
    290                 295                 300

Pro Thr Thr Gly Ser Arg Asn Glu Met Glu Ala Arg Tyr Leu His Tyr
305                 310                 315                 320

Tyr Val Ile Tyr Asn Ala Asn Leu Asp Ser Asn His Pro Val Lys Glu
                325                 330                 335

Ser Ile Leu Arg Gln Gln Leu Lys Gln Trp Glu Met Val Gln His Gln
            340                 345                 350

Pro Ser Phe Gly Asp Ala Glu Trp Lys Gly Ala Glu Thr Gly Asn Trp
        355                 360                 365

Lys Glu Leu Ile Ala Arg Ala Arg Ser Asn
    370                 375
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<210> 89
<211> 764

<212> DNA
<213> Candida albicans

<400> 89
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ttactccaga aacaagaaac acaagacttg tttggtgttg ctattaaaag ataatatata 120
atcaggataa aagaattttt ttggttaaag aaaattacag ggacggtaaa tcattcttct 180
tccctataaa ccaaaaatct tatatgtccc aagttaactt attagaattc caagattatt 240
tactttacag tgaatcatta aacattttaa ttgaaagcga gtttagctca atgtcttcag 300
acacaactgc ttttcaggca ccaccaacaa aagcaccaga agcctccatg gatctgggta 360
caattcccaa aagatctcca gcaagattgt ttcaaaggtg gatatcatca tcatcatcaa 420
aagataagcc agtatatgca gaaaaagccc ttctcaagaa gcaaaacata gcaccggaac 480
caataaaaat aactaaacaa caagtaccag ctaaacaaat aggtacatct gaaccatcgt 540
cgcctctaag tgtggcttcg agtcatgata attcatgttc cgattcaagt gcagcttcta 600
tatttttctga ttctaaaaat aacaatagta tgcaaatgtt actcacagat gatatagagg 660
acatattaga ggacatagac gatgctgaga tatacgatgc tgagaaggtt accataacat 720
atataagttc taaatcatgc taatacacat tattaattat ttga 764

<210> 90
<211> 179
<212> PRT
<213> Candida albicans

<400> 90
Met Ser Gln Val Asn Leu Leu Glu Phe Gln Asp Tyr Leu Leu Tyr Ser
1 5 10 15

Glu Ser Leu Asn Ile Leu Ile Glu Ser Glu Phe Ser Ser Met Ser Ser
20 25 30

Asp Thr Thr Ala Phe Gln Ala Pro Pro Thr Lys Ala Pro Glu Ala Ser
35 40 45

Met Asp Ser Gly Thr Ile Pro Lys Arg Ser Pro Ala Arg Leu Phe Gln
50 55 60

Arg Trp Ile Ser Ser Ser Ser Ser Lys Asp Lys Pro Val Tyr Ala Glu
65 70 75 80

Lys Ala Leu Leu Lys Lys Gln Asn Ile Ala Pro Glu Pro Ile Lys Ile
85 90 95

Thr Lys Gln Gln Val Pro Ala Lys Gln Ile Gly Thr Ser Glu Pro Ser
100 105 110

Ser Pro Leu Ser Val Ala Ser Ser His Asp Asn Ser Cys Ser Asp Ser
115 120 125

Ser Ala Ala Ser Ile Phe Ser Asp Ser Lys Asn Asn Asn Ser Met Gln
130 135 140

Met Leu Leu Thr Asp Asp Ile Glu Asp Ile Leu Glu Asp Ile Asp Asp
145 150 155 160

Ala Glu Ile Tyr Asp Ala Glu Lys Val Thr Ile Thr Tyr Ile Ser Ser
165 170 175

Lys Ser Cys

<210> 91
<211> 2154
<212> DNA
<213> Candida albicans

<400> 91
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ggaattgagt tggagtttag tcaacaaggc agtagcgatg gtgctataga gaaagcggca 120
ttggcagttc ctgtgtttag cgttgacaac caagactttg tattgataag agaccttgcc 180
aagtactggg gctacccttc atcgtatcaa ttgattgtca agttggtcaa atgtgctaac 240
attgaaaagt cgcaaatctt aaagaccgat aaggatttga ataaagagtt gtttgagttg 300
gatttgattg aagaagcaga tacaaagatt gatctttttt atatttcgtt acccttggtc 360
tattcaagaa tagaaaataa gaaggttttt tatgttctgc gtgaaccaga acagccaaag 420
gtgtcgaaag ccccaacaca agagaaacca gcaagtgtgg ttgctgctga agaagatgac 480
gataatctag atgatgatga ggaggacgaa gtggatgaag acatggatga agataatgat 540
aatagtgggg aattgtctaa aggatacaag cacatgcaca aggaccatcc aaagtatata 600
aatgacgata gggttactat tggacaagtg tttcatcaat acggacttga cccttcgaca 660
ccattaaccc attcactttt caatagtatc aactcaatgt cgaagctaaa ctattacaag 720
aattttggag tttcaggtta ccgatttctt cccaacagca agttatctta tgcagaacga 780
gaattggtgt tgaatgccaa caactacaat gatatgcaca ttaacgaaaa gacagaatcc 840
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gatccgaact ccatagattt aagcgagtca gtgattccgg gacaagggtt tatacctgac 960
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ctcccgctgt cgttcaacac aaagaatctt aatgcaactt cgaactcttc gtatttgttt 1080
aatgataatg tcaagataaa gtcaaaaagt attcagaagt tggtgttcaa cagcgatacc 1140
gataattacc atcacacaaa gtatttctac accaaaacct accgtggtcc agggtcgggg 1200
aattacaagg atggtgcatt gatgaacaaa atcaacaaga tacatctttc cagtaataaa 1260
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aacccagcac cacctccaca gccaattgag acaccacagt tggatcttaa caacaagttt 1920
agcttaccaa cagtgtatcc agagattatt cgaaacttgc cattagagtt gcgagggatt 1980
gtccaagaaa gcaaggagga gcttccgcct atcaaaaagc ccatactcta tgtaactaca 2040
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gccaattcgg ttggatggga taactttaaa aaatataaag atagtgatgt atag 2154

<210> 92
<211> 717
<212> PRT
<213> Candida albicans

<400> 92
Met Ser Ile Thr Val Thr Phe Pro Lys Ser Pro Ser Thr Lys Lys Arg
1 5 10 15

Ala Pro Ala Phe Gly Ile Glu Leu Glu Phe Ser Gln Gln Gly Ser Ser
20 25 30

Asp Gly Ala Ile Glu Lys Ala Ala Leu Ala Val Pro Val Phe Ser Val
35 40 45

Asp Asn Gln Asp Phe Val Leu Ile Arg Asp Leu Ala Lys Tyr Trp Gly
50 55 60

Tyr Pro Ser Ser Tyr Gln Leu Ile Val Lys Leu Val Lys Cys Ala Asn
65 70 75 80

Ile Glu Lys Ser Gln Ile Leu Lys Thr Asp Lys Asp Leu Asn Lys Glu
85 90 95

Leu Phe Glu Leu Asp Leu Ile Glu Glu Ala Asp Thr Lys Ile Asp Leu
100 105 110

Phe Tyr Ile Ser Leu Pro Leu Val Tyr Ser Arg Ile Glu Asn Lys Lys
115 120 125

Val Phe Tyr Val Ser Arg Glu Pro Glu Gln Pro Lys Val Ser Lys Ala
130 135 140

Pro Thr Gln Glu Lys Pro Ala Ser Val Val Ala Ala Glu Glu Asp Asp
145 150 155 160

Asp Asn Leu Asp Asp Asp Glu Glu Asp Glu Val Asp Glu Asp Met Asp
165 170 175

Glu Asp Asn Asp Asn Ser Gly Glu Leu Ser Lys Gly Tyr Lys His Met

180 185 190

His Lys Asp His Pro Lys Tyr Ile Asn Asp Asp Arg Val Thr Ile Gly
195 200 205

Gln Val Phe His Gln Tyr Gly Leu Asp Pro Ser Thr Pro Leu Thr His
210 215 220

Ser Leu Phe Asn Ser Ile Asn Ser Met Ser Lys Leu Asn Tyr Tyr Lys
225 230 235 240

Asn Phe Gly Val Ser Gly Tyr Arg Phe Leu Pro Asn Ser Lys Leu Ser
245 250 255

Tyr Ala Glu Arg Glu Leu Val Leu Asn Ala Asn Asn Tyr Asn Asp Met
260 265 270

His Ile Asn Glu Lys Thr Glu Ser Lys Pro Lys Lys Ser Phe Arg Lys
275 280 285

Pro Ile Gly Lys Ser Lys Lys His Asn Leu Gln Ile Asp Pro Asn Ser
290 295 300

Ile Asp Leu Ser Glu Ser Val Ile Pro Gly Gln Gly Phe Ile Pro Asp
305 310 315 320

Phe Ser Ile His His Leu Cys Lys Val Pro Asn Tyr Tyr Val Thr Ser
325 330 335

Asn His Gln Ser Leu Pro Ser Ser Phe Asn Thr Lys Asn Leu Asn Ala
340 345 350

Thr Ser Asn Ser Ser Tyr Leu Phe Asn Asp Asn Val Lys Ile Lys Ser
355 360 365

Lys Ser Ile Gln Lys Leu Val Phe Asn Ser Asp Thr Asp Asn Tyr His
370 375 380

His Thr Lys Tyr Phe Tyr Thr Lys Thr Tyr Arg Gly Pro Gly Ser Gly
385 390 395 400

Asn Tyr Lys Asp Gly Ala Leu Met Asn Lys Ile Asn Lys Ile His Leu
405 410 415

Ser Ser Asn Lys Lys Pro Arg His Lys Arg Lys Val Ser Asn Asn Asn
420 425 430

Arg Tyr Asn Lys Ser Leu Lys Gly Leu Val His Glu Lys Phe Asp Lys

435 440 445

Asn Phe Val Glu Tyr Leu Leu Ser Glu Gln Arg Lys Tyr Thr Glu Asp
450 455 460

Tyr Ser Asn Leu Glu Ile Leu His Asn Ser Leu Gln Phe Asn Val Leu
465 470 475 480

Leu Asn Thr Tyr Arg Gly Val Ala Gln Glu Thr Trp Asn Asn Tyr Tyr
485 490 495

Lys Phe Lys Leu Ile Asp Phe Glu Gln Leu Lys Ala Leu Gln Met Glu
500 505 510

Ala Asn Glu Leu Glu Glu Arg Lys Leu Asp Ala Ala Arg His Gln Gln
515 520 525

Trp Ala Glu Glu Glu Lys Leu Arg Gln Glu Arg Leu Arg Leu Val Phe
530 535 540

Glu Asp Glu Arg Asn Glu Phe Glu Gln Leu Gln Ser Glu Phe Gly Gln
545 550 555 560

Arg Lys Lys Asp Leu Tyr Glu Lys Leu Arg Arg Arg Gln Leu Glu Ala
565 570 575

Ser Leu Ser Asp Ser Phe Glu Ala Asp Ser Glu Asn Asp Asp Glu Ser
580 585 590

Glu Leu Ala Gln Ile Gln Gln Asp Phe Glu Ser Ser Ala Asn Ala Leu
595 600 605

Lys Thr Lys Phe Glu Ala Lys Arg Lys Asp Leu Ile Asn Pro Ala Pro
610 615 620

Pro Pro Gln Pro Ile Glu Thr Pro Gln Leu Asp Leu Asn Asn Lys Phe
625 630 635 640

Ser Leu Pro Thr Val Tyr Pro Glu Ile Ile Arg Asn Leu Pro Leu Glu
645 650 655

Leu Arg Gly Ile Val Gln Glu Ser Lys Glu Glu Leu Pro Pro Ile Lys
660 665 670

Lys Pro Ile Leu Tyr Val Thr Thr Tyr Pro Glu Arg Pro Asn Pro Glu
675 680 685

Tyr Leu Thr Arg Ile Glu Ile Ile Lys Leu Pro Asn Ala Asn Ser Val

690 695 700

Gly Trp Asp Asn Phe Lys Lys Tyr Lys Asp Ser Asp Val
705 710 715

<210> 93
<211> 411
<212> DNA
<213> Candida albicans

<400> 93
atgaatagat tcttattcaa ctgtttatta ttcattggtt tacttttaat atacaaatat 60
ttattcatgt ctgctgatgg taagaaagaa gatattcttg aaactggtga gaaaattgat 120
ggggaattac aagttaaatt aggagataaa ttctttccca tttcaagatt tgctaaacct 180
catgctgttg ttcaccctgc tgatcaccat tcgaaagttg atgccaacaa gttccccgat 240
gttgaaccag aacaaaaaca aaaagaggat ttaaaagagt ttaaccaaca agtcttaaag 300
cctgacatta ataaaccaaa ggttgatcct aattcatttc cagatattga accagaggct 360
aaagaaagag aagccaaatt aaaagctgaa agacttaaaa agagccaata a 411

<210> 94
<211> 136
<212> PRT
<213> Candida albicans

<400> 94
Met Asn Arg Phe Leu Phe Asn Cys Leu Leu Phe Ile Gly Leu Leu Leu
1 5 10 15

Ile Tyr Lys Tyr Leu Phe Met Ser Ala Asp Gly Lys Lys Glu Asp Ile
20 25 30

Leu Glu Thr Gly Glu Lys Ile Asp Gly Glu Leu Gln Val Lys Leu Gly
35 40 45

Asp Lys Phe Phe Pro Ile Ser Arg Phe Ala Lys Pro His Ala Val Val
50 55 60

His Pro Ala Asp His His Ser Lys Val Asp Ala Asn Lys Phe Pro Asp
65 70 75 80

Val Glu Pro Glu Gln Lys Gln Lys Glu Asp Leu Lys Glu Phe Asn Gln
85 90 95

Gln Val Leu Lys Pro Asp Ile Asn Lys Pro Lys Val Asp Pro Asn Ser
100 105 110

Phe Pro Asp Ile Glu Pro Glu Ala Lys Glu Arg Glu Ala Lys Leu Lys

115 120 125

Ala Glu Arg Leu Lys Lys Ser Gln
130 135

<210> 95
<211> 1193
<212> DNA
<213> Candida albicans

<400> 95
tgacataaaa cgtgtaacca ctacccaaaa gtgtatgttt aaaatactgt ataaacaaaa 60
ccaccctatt ctctgaacat tgaatcaact ttaagtttac tgttgtataa tttaagcaaa 120
actttgcttc aaattcatat taaaatttta aaaacaattg atccatccat atttctttgc 180
tgccagccat cttctttttc tggttaagtc ttacacgact caagtgtgta aagttttttt 240
tttttgctac acgtcttgaa tttttttttcc tttcagaaat tttatatatt gaagccaatt 300
tcatttcgaa cttaatcatt tttttttata aatatttagc aaaataatta gccatatcaa 360
ttacaaataa tttttacatt tgaataaacc cagataaact ttcaaatcca tcctagcacc 420
ttcataatcc attctatata tttgcttctt tattgtctac agtcatttcc gttgcaatgt 480
cctcttctaa tgatacacca tctttatttg tcacaccaca aacaccacca agacagcaac 540
aaaggagaaa aagtaataca ggagctatat ctacacccgt tgcctcatca gtattattaa 600
ctccatctac aacaacaaaa aaacctacaa gaactccagt atcacagaaa agaaaacaag 660
gtgtacagtt gtctccacca caggcaaaca aattcccctt tactccaatc acccctcaaa 720
aatcaccatg caagacaaga aagaatttgg atttattcac tagtaacgaa aaatttggct 780
tattgttacc atcgccatcc actattggtt ctggtagatg tcataactct ttcacgcaag 840
ctccacctcc attatttgat ttgaagaagg ttaatgagtt taaagtacct aagacacccg 900
caaaacaaat tatagacaac tctagaacaa aagaatcaga aaatgaagat gactgggaag 960
tgatggacat agatgaagtt gccaaaattc ctcgtgcaaa gttgaggaac ccttttatag 1020
acacttttga accaacgagt ccggttacac ctgaggagag tactggagat agaattaact 1080
atgacacaca tatggaattg ataaacagta aaactggtaa gaaaagagtt gtaaagttaa 1140
caaagaatca aatgaaaatc aaaccaaaga gattatcgtt tgataatata taa 1193

<210> 96
<211> 238
<212> PRT
<213> Candida albicans

<400> 96
Met Ser Ser Ser Asn Asp Thr Pro Ser Leu Phe Val Thr Pro Gln Thr
1 5 10 15

Pro Pro Arg Gln Gln Gln Arg Arg Lys Ser Asn Thr Gly Ala Ile Ser
20 25 30

Thr Pro Val Ala Ser Ser Val Leu Leu Thr Pro Ser Thr Thr Thr Lys
35 40 45

Lys Pro Thr Arg Thr Pro Val Ser Gln Lys Arg Lys Gln Gly Val Gln
50 55 60

Leu Ser Pro Pro Gln Ala Asn Lys Phe Pro Phe Thr Pro Ile Thr Pro
65 70 75 80

Gln Lys Ser Pro Cys Lys Thr Arg Lys Asn Leu Asp Leu Phe Thr Ser
85 90 95

Asn Glu Lys Phe Gly Leu Leu Leu Pro Ser Pro Ser Thr Ile Gly Ser
100 105 110

Gly Arg Cys His Asn Ser Phe Thr Gln Ala Pro Pro Pro Leu Phe Asp
115 120 125

Leu Lys Lys Val Asn Glu Phe Lys Val Pro Lys Thr Pro Ala Lys Gln
130 135 140

Ile Ile Asp Asn Ser Arg Thr Lys Glu Ser Glu Asn Glu Asp Asp Trp
145 150 155 160

Glu Val Met Asp Ile Asp Glu Val Ala Lys Ile Pro Arg Ala Lys Leu
165 170 175

Arg Asn Pro Phe Ile Asp Thr Phe Glu Pro Thr Ser Pro Val Thr Pro
180 185 190

Glu Glu Ser Thr Gly Asp Arg Ile Asn Tyr Asp Thr His Met Glu Leu
195 200 205

Ile Asn Ser Lys Thr Gly Lys Lys Arg Val Val Lys Leu Thr Lys Asn
210 215 220

Gln Met Lys Ile Lys Pro Lys Arg Leu Ser Phe Asp Asn Ile
225 230 235

<210> 97
<211> 888
<212> DNA
<213> Candida albicans

<400> 97
atgcaattct catccgctgt cgtcttatcc gctgttgctg gttccgcttt ggctgcttac 60
tccaactcca ctgttactga cattcaaacc actgttgtca ccatcacttc atgtgaagaa 120
aacaaatgtc acgaaactga agttaccact ggtgttacca ccgtcactga agttgacact 180
acgtacacca cctactgccc attgtcaacc actgaagctc cagctccatc tactgctact 240
gatgtttcta ccaccgttgt caccatcacc tcatgtgaag aagacaaatg tcacgaaacc 300

gctgtcacca ccggtgtcac cactgtcact gaaggtacta ccatctacac tacctactgc 360
ccattgccat ctactgaagc tccaggtcca gctccatcta ctgctgaaga atctaaacca 420
gctgaatctt ccccagttcc aaccaccgct gctgaatctt ccccagctaa aactactgct 480
gctgaatctt ccccagctca agaaaccact ccaaagaccg ttgctgctga atcttcttca 540
gctgaaacta ctgctccagc tgtctctacc gctgaagccg gtgctgctgc taacgctgtc 600
ccagttgctg ctggtttgtt ggctttggct gctttgtttt aagtttacta gagcttaaat 660
caaatattta caaacaaaat tttcattttc ccccttttcc ctttcttcat tcttcaaaaa 720
aagggttatt tactattaat tgataaattt atggtttcat gttaatgtac ccttttttt 780
ataaacattg ttattattat tatcatcatt agtttattta tattttcgtg aggttttccg 840
gtttaattaa attttttgga tacatattaa aaatttattt ggtactag 888

<210> 98
<211> 213
<212> PRT
<213> Candida albicans

<400> 98
Met Gln Phe Ser Ser Ala Val Val Leu Ser Ala Val Ala Gly Ser Ala
1 5 10 15

Leu Ala Ala Tyr Ser Asn Ser Thr Val Thr Asp Ile Gln Thr Thr Val
20 25 30

Val Thr Ile Thr Ser Cys Glu Glu Asn Lys Cys His Glu Thr Glu Val
35 40 45

Thr Thr Gly Val Thr Thr Val Thr Glu Val Asp Thr Thr Tyr Thr Thr
50 55 60

Tyr Cys Pro Leu Ser Thr Thr Glu Ala Pro Ala Pro Ser Thr Ala Thr
65 70 75 80

Asp Val Ser Thr Thr Val Val Thr Ile Thr Ser Cys Glu Glu Asp Lys
85 90 95

Cys His Glu Thr Ala Val Thr Thr Gly Val Thr Thr Val Thr Glu Gly
100 105 110

Thr Thr Ile Tyr Thr Thr Tyr Cys Pro Leu Pro Ser Thr Glu Ala Pro
115 120 125

Gly Pro Ala Pro Ser Thr Ala Glu Glu Ser Lys Pro Ala Glu Ser Ser
130 135 140

Pro Val Pro Thr Thr Ala Ala Glu Ser Ser Pro Ala Lys Thr Thr Ala
145 150 155 160

Ala Glu Ser Ser Pro Ala Gln Glu Thr Thr Pro Lys Thr Val Ala Ala

165 170 175

Glu S r Ser Ser Ala Glu Thr Thr Ala Pro Ala Val Ser Thr Ala Glu
180 185 190

Ala Gly Ala Ala Ala Asn Ala Val Pro Val Ala Ala Gly Leu Leu Ala
195 200 205

Leu Ala Ala Leu Phe
210

<210> 99
<211> 977
<212> DNA
<213> Candida albicans

<400> 99
cacattcaac tttacttctt cattatcatt gctaatccat cttatatcaa gtttagatta 60
attgttatta aattttccaa cttctatata ctcaatctta gacaaccaca ccacaccaaa 120
ttacaccacc tataaatata aacaatgtca aaagacgaat atttcggtaa acctagtggt 180
ccaccaccaa attataataa tcaaccccaa tcacaacaac cacaacaaag ttatgtacca 240
caatcacaac ccaattattc tcaacaaaca caagatcgag ggatgtttag tggtggtggt 300
ggtggtcatg gccactatca acaacaacaa ggatataatg cttatggacc accacctcca 360
caaggtggat attatcaaca acagccaggt ggtggtggtg gatattatca acaacaacaa 420
caacaacaac ctatgtatgt acaacaacaa ccacgttctg gaggtaatga ttcttgttta 480
atgggttgtc ttgctgcatt atgtgtttgc tgtactttag atatgctttt ttaagccaga 540
tatatctact acccgtcttg ttgtttttttc ttcttctata ttcgttgtct tccccccccct 600
ttttttgttt tgttaaattc gtttattatt actattatta taattgttat ttttaaagtt 660
ttatttaata ttattgctaa tattactgct attacgacta tatcactttc aagaaatgaa 720
atgaaattta atttaattac aagatttgtt gaaatctttc ctttttttttt ttttttttg 780
ctatttaatt aatttacata taaaggtttt actcctattc cttttgagta tgttattata 840
attaatggtt attaatatat tcttcaatta agttccacta tgatgttttg gtggtggtgg 900
tggtggtgat agtagtttac tttttgtttt tttgtgttca aattttaaaa agagatctaa 960
ctatattgta aaaaaaa 977

<210> 100
<211> 129
<212> PRT
<213> Candida albicans

<400> 100
Met Ser Lys Asp Glu Tyr Phe Gly Lys Pro Ser Gly Pro Pro Pro Asn
1 5 10 15

Tyr Asn Asn Gln Pro Gln Ser Gln Gln Pro Gln Gln Ser Tyr Val Pro
20 25 30

Gln Ser Gln Pro Asn Tyr Ser Gln Gln Thr Gln Asp Arg Gly Met Phe
35 40 45

Ser Gly Gly Gly Gly Gly His Gly His Tyr Gln Gln Gln Gln Gly Tyr
50 55 60

Asn Ala Tyr Gly Pro Pro Pro Pro Gln Gly Gly Tyr Tyr Gln Gln Gln
65 70 75 80

Pro Gly Gly Gly Gly Gly Tyr Tyr Gln Gln Gln Gln Gln Gln Gln Pro
85 90 95

Met Tyr Val Gln Gln Gln Pro Arg Ser Gly Gly Asn Asp Ser Cys Leu
100 105 110

Met Gly Cys Leu Ala Ala Leu Cys Val Cys Cys Thr Leu Asp Met Leu
115 120 125

Phe

<210> 101
<211> 2994
<212> DNA
<213> Candida albicans

<400> 101
atgactttac caattcagga tttagaacct gattattata tttccgtcaa ttatcctacc 60
accgataatg gatcaccaac cccacaagct gaaaaatcat tgaaaacatt aattgattta 120
ttatacgata aagggtttgc cgcccaaatt agacctggtg atttagacca tttgttagtc 180
tttgttaaat tgtcttcata caagttttct gaagaagctg aaaaagattt aattaaaaat 240
tatgaatttg gtgtcacggg taaagatgac gtgttagctt ctaaacttag aattatttat 300
caatacttaa cttatccaca atcagttggt ggatgtggta ttactcctaa ttctggggat 360
tggaaatttg tcaccagtat tgttccaatt actaatgcct ttaatgaaac cactttagtt 420
gaagatttaa aaattaatgt tactcaacca aatttatcaa ttgccactat caaaaagaca 480
tatggagttg aagttgctct ttattttgaa tatataaaac attacacttt ttggttatta 540
ttgctttcta ttattggtct tgtatctcat tttagaaaag ataaacgatt cctgttaact 600
tttgccttta tcaatttgct ttgggggttt ttattccttg catcatggca tagaagagaa 660
caacatttgg ttaatgtatg gggtgttcaa aatagtcatt taattgaaga acataattcc 720
gaattggcta aagtcaatga aagatatgaa gaaaaatcaa cttatttcca tgcaaataat 780
accaatggat tcagattttt aaaacaattg gcatttatcc ccattgcctt ggtgtttgtt 840
ggtgttttga ttagttatca attgagttgt ttctgtattg aaatcttttt aaccgatatt 900
tatgatggcc ccgggaaatc tttattgact ttattaccaa cggttttaat cagtgtattt 960
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gtgcaacctc atttaggtga tattaaaacc actattgcca catatgcttg tgaaaatatga 1200

ttctacacca aatacttgtt gaaattaaag agtcaagaag aatttaaaat caatcaaggt 1260
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gtcagattat cgttgaaact tcctgaatat aatgttgatg atgattttag aggattagtt 1500
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gttgataatg atattaaatt gagacatgat tattattctg ggaaagtaaa accaacttat 1980
aaagtccact cggatgagtt gtgggagaag tttaccccac aatcaacttt gaatttcact 2040
gttcctaaac caaccgcaga aactgatgat aaagttgaaa aaattgcttc taccgaaggt 2100
gcttatctga cttctgcaga aaaatctact actactgcta cttctcgttc tgataagagt 2160
aaaattcttg ctgaaaagga agctattttg aaacaaaagg aagctgagtt ggccgaatta 2220
gaaaagaaaa agaccaaact aaatgatttt aaagatccaa ccgattctgt cattaaaacc 2280
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gatattgatc cagatgccgc cgccgcagca actgcaacat ctactgctaa tgattctggt 2400
gcaaaaaaat caacatcaac atcaacatca gcagccacag atactactaa cactgcccca 2460
tctcattctg gtccaactcc tgtcacttct tctgaaaaat caaacaacaa caacaacagt 2520
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tataaattgt atgaattcca gttttttat ttttatttta ttttatttta gtttagtttt 2940
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<210> 102
<211> 952
<212> PRT
<213> Candida albicans

<400> 102
Met Thr Leu Pro Ile Gln Asp Leu Glu Pro Asp Tyr Tyr Ile Ser Val
1 5 10 15

Asn Tyr Pro Thr Thr Asp Asn Gly Ser Pro Thr Pro Gln Ala Glu Lys
20 25 30

Ser Leu Lys Thr Leu Ile Asp Leu Leu Tyr Asp Lys Gly Phe Ala Ala
35 40 45

Gln Ile Arg Pro Gly Asp Leu Asp His Leu Leu Val Phe Val Lys Leu
50 55 60

Ser Ser Tyr Lys Phe Ser Glu Glu Ala Glu Lys Asp Leu Ile Lys Asn
65 70 75 80

Tyr Glu Phe Gly Val Thr Gly Lys Asp Asp Val Leu Ala Ser Lys Leu
85 90 95

Arg Ile Ile Tyr Gln Tyr Leu Thr Tyr Pro Gln Ser Val Gly Gly Cys
100 105 110

Gly Ile Thr Pro Asn Ser Gly Asp Trp Lys Phe Val Thr Ser Ile Val
115 120 125

Pro Ile Thr Asn Ala Phe Asn Glu Thr Thr Leu Val Glu Asp Leu Lys
130 135 140

Ile Asn Val Thr Gln Pro Asn Leu Ser Ile Ala Thr Ile Lys Lys Thr
145 150 155 160

Tyr Gly Val Glu Val Ala Leu Tyr Phe Glu Tyr Ile Lys His Tyr Thr
165 170 175

Phe Trp Leu Leu Leu Leu Ser Ile Ile Gly Leu Val Ser His Phe Arg
180 185 190

Lys Asp Lys Arg Phe Ser Leu Thr Phe Ala Phe Ile Asn Leu Leu Trp
195 200 205

Gly Val Leu Phe Leu Ala Ser Trp His Arg Arg Glu Gln His Leu Val
210 215 220

Asn Val Trp Gly Val Gln Asn Ser His Leu Ile Glu Glu His Asn Ser
225 230 235 240

Glu Leu Ala Lys Val Asn Glu Arg Tyr Glu Glu Lys Ser Thr Tyr Phe
245 250 255

His Ala Asn Asn Thr Asn Gly Phe Arg Phe Leu Lys Gln Leu Ala Phe
260 265 270

Ile Pro Ile Ala Leu Val Phe Val Gly Val Leu Ile Ser Tyr Gln Leu
275 280 285

Ser Cys Phe Cys Ile Glu Ile Phe Leu Thr Asp Ile Tyr Asp Gly Pro
290 295 300

Gly Lys Ser Leu Leu Thr Leu Leu Pro Thr Val Leu Ile Ser Val Phe
305 310 315 320

Val Pro Ile Leu Thr Ile Val Tyr Asn Ala Val Thr Asp Ile Ile Ile
325 330 335

Lys Trp Glu Asn His Asp Asn Gln Tyr Ser Lys Asn Asn Ser Ile Leu
340 345 350

Val Lys Thr Phe Val Leu Asn Phe Leu Thr Gly Tyr Val Pro Leu Ile
355 360 365

Ile Thr Ser Phe Ile Tyr Leu Pro Phe Ala His Leu Val Gln Pro His
370 375 380

Leu Gly Asp Ile Lys Thr Thr Ile Ala Thr Tyr Ala Gly Glu Asn Arg
385 390 395 400

Phe Tyr Thr Lys Tyr Leu Leu Lys Leu Lys Ser Gln Glu Glu Phe Lys
405 410 415

Ile Asn Gln Gly Arg Leu Asp Ala Gln Phe Phe Tyr Phe Ile Val Thr
420 425 430

Asn Gln Val Ile Gln Leu Val Leu Lys Tyr Ile Leu Pro Leu Gly Leu
435 440 445

Arg Phe Val Phe Asn Phe Ile Glu Thr Lys Ile Gln Lys Lys Pro Gln
450 455 460

Leu Gln Thr Lys Asp Asp Asn Pro Asp Glu Ser Ile Trp Leu His Asn
465 470 475 480

Val Arg Leu Ser Leu Lys Leu Pro Glu Tyr Asn Val Asp Asp Asp Phe
485 490 495

Arg Gly Leu Val Leu Gln Phe Gly Tyr Leu Ile Met Phe Gly Pro Val
500 505 510

Trp Pro Leu Ala Pro Leu Val Cys Ile Ile Phe Asn Leu Ile Phe Phe
515 520 525

Lys Leu Asp Asn Phe Lys Leu Leu Asn Gly Lys Tyr Phe Lys Pro Pro
530 535 540

Val Pro Arg Arg Val Asp Ser Ile His Pro Trp Asn Leu Ala Leu Phe
545 550 555 560

Leu Leu Ala Trp Ile Gly Ser Ile Ile Ser Pro Val Val Thr Ala Phe
565 570 575

Tyr Arg His Gly Thr Ala Pro Pro Lys Ser Met Gly Gln Phe Ala Leu
580 585 590

Asp Lys Ala Ser Val His Val Ser Ser Ser Val Phe Leu Val Leu Leu
595 600 605

Met Phe Val Ser Glu His Gly Phe Leu Ile Leu Ser Tyr Leu Leu Phe
610 615 620

Glu Phe Ser Ser Leu Phe Lys Ser Gln Val Glu Trp Glu Asn Asp Phe
625 630 635 640

Val Asp Asn Asp Ile Lys Leu Arg His Asp Tyr Tyr Ser Gly Lys Val
645 650 655

Lys Pro Thr Tyr Lys Val His Ser Asp Glu Leu Trp Glu Lys Phe Thr
660 665 670

Pro Gln Ser Thr Leu Asn Phe Thr Val Pro Lys Pro Thr Ala Glu Thr
675 680 685

Asp Asp Lys Val Glu Lys Ile Ala Ser Thr Glu Gly Ala Tyr Ser Thr
690 695 700

Ser Ala Glu Lys Ser Thr Thr Thr Ala Thr Ser Arg Ser Asp Lys Ser
705 710 715 720

Lys Ile Leu Ala Glu Lys Glu Ala Ile Leu Lys Gln Lys Glu Ala Glu
725 730 735

Leu Ala Glu Leu Glu Lys Lys Lys Thr Lys Leu Asn Asp Phe Lys Asp
740 745 750

Pro Thr Asp Ser Val Ile Lys Thr Lys Ser Ser Ala Asn Gly Lys Ala
755 760 765

Val Leu Ser Thr Ile Asp Asn Asn Lys His Val Ser Asp Ile Asp Pro
770 775 780

Asp Ala Ala Ala Ala Ala Thr Ala Thr Ser Thr Ala Asn Asp Ser Gly
785 790 795 800

Ala Lys Lys Ser Thr Ser Thr Ser Thr Ser Ala Ala Thr Asp Thr Thr
805 810 815

Asn Thr Ala Pro Ser His Ser Gly Pro Thr Pro Val Thr Ser Ser Glu
820 825 830

Lys S r Asn Asn Asn Asn Ser Lys Pro S r Asp Ser Thr Lys Ser
835 840 845

Thr Leu Ala Asn Asp Glu Thr Arg Lys Thr Leu Asp Pro Lys Gly Val
850 855 860

Gly Ser Thr Thr Thr Gly Asp Lys Asp Thr Val Ser Ser Asp Lys Ala
865 870 875 880

Ser Ser Pro Ile Glu Asp Lys Glu Ser Ser Pro Ser Leu Ala Gly Ser
885 890 895

Ser Thr Ser Thr Pro Ser Gly Thr Asp Lys Lys Thr Ser Pro Lys Lys
900 905 910

Leu Val Thr Asn Ala Val Asn Lys Val Glu Asn Asn Asp Asp Phe Lys
915 920 925

Lys Phe Ile Asn Glu Ala Glu Lys Glu Ala Lys Lys Ser Lys Ser Gly
930 935 940

Leu Lys Lys Leu Phe Asn Lys Lys
945 950

<210> 103
<211> 72
<212> PRT
<213> Candida albicans

<400> 103
Met Leu Val Ile Leu Ile Gln Met Pro Pro Pro Gln Gln Ser Gln His
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Leu Ser Leu Met Ile Ser Val Gln Lys Asn Gln His Gln His Gln His
20 25 30

Gln Gln Pro Gln Ile Leu Leu Thr Ser Pro His Leu Ile Ser Val Gln
35 40 45

Leu Ser Ser Leu Leu Ser Lys Asn Gln Thr Thr Thr Thr Thr Val Ser
50 55 60

Gln Val Ile Val Pro Asn Leu Leu
65 70

<210> 104
<211> 4809
<212> DNA
<213> Candida albicans

<400> 104
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tacaaactcg caagaaagca ttttgaaacc agtgttgccc ttttaaaagc cttcacattg 180
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<210> 105
<211> 1603
<212> PRT
<213> Candida albicans

<400> 105
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Leu Gly Lys Glu Ile Asp Leu Lys Asp Phe Arg Arg Gly Ile S r Phe
20 25 30

Lys Val Phe Asp Phe Ser Val Thr Tyr Lys Leu Ala Arg Lys His Phe
35 40 45

Glu Thr Ser Val Ala Leu Leu Lys Ala Phe Thr Leu Ser Glu Tyr Ala
50 55 60

Ser Glu Tyr Ile Glu Asp Phe Asp Lys Val Thr Glu Val Gln Val Ser
65 70 75 80

Glu Ser Glu Ile Ser Asp Leu Ser Ser Ile Asn Ser Ala Glu Ser Ile
85 90 95

Pro Leu Asn Asp Ala Ser Pro Ser Glu Leu Asp Glu Ser Asn Thr Lys
100 105 110

Lys Ile Lys Thr Val Leu Thr Val Arg Asp Ile Leu Val Ser Asn Ala
115 120 125

Gly Lys Ser Asp Glu Lys Asp Pro Asp Arg Leu Thr Leu Ser Ile Pro
130 135 140

Glu Val Asp Gly Arg Val Asp Met Phe Leu Val Trp Cys Cys Phe Tyr
145 150 155 160

Ala Lys Thr Met Leu Glu Arg Phe Lys Pro Thr Val Glu Ser Ser Cys
165 170 175

Thr Lys Asn Gln Ile Lys Ile Ile Arg Gly Pro Arg Lys Lys Leu Lys
180 185 190

Leu Asp Val His Leu Asp Ser Val Ala Leu Val Ile Arg Leu Pro Arg
195 200 205

Lys Val Asp Val Met Ile Glu Ile Asp Arg Ala Arg Leu Lys Asn Ala
210 215 220

Leu Val Leu Lys Ser Ala Asp Ile Val Asn Cys Arg Leu Tyr Val Val
225 230 235 240

Asp Pro Ser Thr Lys Phe Trp Ala Arg Leu Leu Ile Ile Lys Glu Pro
245 250 255

Lys Phe Ser Ile Asp Phe Thr Lys Ser Ile His Asp Ala Tyr Phe Gly
260 265 270

Ile Ser Thr Arg Ser Ile Arg Ile Ser Val Pro Asn Arg Phe Leu Phe
275 280 285

Tyr Thr Val Ile Asp Asn Phe Ile Thr Phe Phe Lys Ala Ile Lys Gln
290 295 300

Leu Ser Gln Asn Phe Arg Tyr Phe Asn Trp Gly Ile Asp Glu Phe Glu
305 310 315 320

Thr Ile Tyr Pro Ser Gln Lys Asn Ala Ile Val Phe Pro His Val Asn
325 330 335

Ile Lys Thr Ala Val Leu Gly Met Glu Leu Arg Ala Asp Pro Phe Glu
340 345 350

Asn Lys Leu Ala Leu Ile Phe Glu Leu Gly Lys Ile Glu Gln Lys Glu
355 360 365

Arg Ile Arg Lys Trp Lys Ala Phe Glu Lys Lys Ser Gln Glu Ile Leu
370 375 380

Asp Gly Val Glu Ser Asn Ile Glu Asp Gln Ile Glu Leu Ser Asn Ile
385 390 395 400

Ala Ala Pro Ile Pro Ser Pro Ala Pro Ile Ala Ser Lys Thr Thr Thr
405 410 415

Ser Thr Met Thr Pro Asn Val Ala Gly Asp Ser Ile Thr Arg Pro Asp
420 425 430

Ser Pro Pro Arg Ser Gly Ser Ser Glu Cys Ser Phe Thr Ser Gly Ala
435 440 445

Gly Leu Ile Lys Asn Lys Leu Leu Asn Arg Lys Lys Pro Thr Lys Thr
450 455 460

Ser Val Asn Gly Val Ala Pro Val Asn Glu Ile Glu Pro Ala Asp Ala
465 470 475 480

Lys Tyr Thr Val Glu Glu Ala Glu Glu Arg Ile Ala Glu Ala Lys Glu
485 490 495

Arg Leu Phe Glu Asn Phe Ser Lys Ser Trp Cys Arg Lys Tyr Arg Val
500 505 510

Phe Glu Glu Thr Lys Cys Arg Lys Trp Lys Glu Arg Gly Glu Asn Ile
515 520 525

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Trp Gly Ser His Asp Ile Asn Glu Val Met Lys Glu Lys Tyr Asp Ile
    530                 535                 540

Val Glu Tyr Asp His Gly Lys Pro Leu Thr Gly Ala Ile Phe Arg Asp
545                 550                 555                 560
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Leu Lys Met Asn Gln Ala Glu Val Asn Ile Glu Asn Ala Asp Ala Arg
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Val Ile Tyr Ala Leu Phe Asn Asp Thr Ser Val Thr Gly Lys Leu Met
1060 1065 1070

Thr Tyr Leu Asn Ala Asp Ser Ser Asp Ser Ser Thr Asp Gly Ser Gln
1075 1080 1085

Ser Ser Asp Tyr Arg Gly Ser Ser Tyr Ser Arg Trp Leu Glu Asn Val
1090 1095 1100

Glu Ile Ser Asp Gly Asp Phe Ser Trp Tyr Asp Pro Lys Asp Phe Ile
1105 1110 1115 1120

Glu Leu Glu Val Arg Glu Pro Leu Ser Pro Tyr Pro Lys Thr Lys Ile
1125 1130 1135

Leu Pro Phe Phe Ala Thr Pro Lys Phe Ser Tyr Tyr Arg Glu Phe Thr
1140 1145 1150

Leu Gln Lys Asp Gly Pro Phe Pro Phe Gly Ser Glu Lys Ile His Asp
1155 1160 1165

Cys Ile Met Asn Leu Asp Lys Pro Ala Ile Val Gln Ser Arg Ile Leu
1170 1175 1180

Leu Asp Arg Leu Gln Asn Leu Glu Asp Glu Leu Ala His Asn Glu Glu
1185 1190 1195 1200

Met Leu Arg Arg Phe Lys Ile Gln Asn Gly Pro Glu Phe Gln His Asp
1205 1210 1215

Ile Arg Met Thr Glu Gln Glu Ile Ser Thr Leu Lys Glu Lys Val Glu
1220 1225 1230

Val Val Arg Ala Ala Tyr Asn Gly Phe Ser Asp Asp Glu Phe Gly Gly
1235 1240 1245

Leu Pro Ser Ser Ser Ala Asn Asn Val Ala Asp Asp Asp Asp Gly Ser
1250 1255 1260

Ser Ser Leu Ser Arg Ser Ser Thr Gly Leu Ser Ala Tyr Ser Ser His
1265 1270 1275 1280

Val Thr Gln Asp Gln Met Ser Gln Ala Ala Ala Phe Val Ser Ile Ala
1285 1290 1295

<210> 113
<211> 2021
<212> DNA
<213> Candida albicans

<400> 113
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gacgtcactg aaacagggga cggatcatta gaggattttg ttgaacattt tactgatgga 180
caagttcaat ttggtttagc cagggttact gttccaggat ctgacgtttc caaaaacatc 240
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gatgatttag acgtgaatga attcttgaat agagttggtg ctgctgctgg tgcaagatat 420
tccactcaaa cttccggact caaaaaacca tcccctgctg cacctaaacc tacttcaaaa 480
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gatgctgaag acgttgagga aagagacttt gacaagaaac ctttggataa cgttccatcg 660
gcatataaac caacaaaggt taacattgac gaattgagaa aacaaaaatc agatacaact 720
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<210> 114
<211> 648
<212> PRT
<213> Candida albicans

<400> 114
Met Glu Lys Ile Asp Il Asn Thr Asn Ser Asn Lys Ile Gln Gln Ala

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20 25 30

Ser Val Asp Lys Asn Ala Thr Met Asp Val Thr Glu Thr Gly Asp Gly
35 40 45

Ser Leu Glu Asp Phe Val Glu His Phe Thr Asp Gly Gln Val Gln Phe
50 55 60

Gly Leu Ala Arg Val Thr Val Pro Gly Ser Asp Val Ser Lys Asn Ile
65 70 75 80

Leu Leu Gly Trp Cys Pro Asp Ser Ala Pro Ala Lys Leu Arg Leu Ser
85 90 95

Phe Ala Asn Asn Phe Ala Asp Val Ser Arg Val Leu Ser Gly Tyr His
100 105 110

Val Gln Ile Thr Ala Arg Asp Gln Asp Asp Leu Asp Val Asn Glu Phe
115 120 125

Leu Asn Arg Val Gly Ala Ala Ala Gly Ala Arg Tyr Ser Thr Gln Thr
130 135 140

Ser Gly Leu Lys Lys Pro Ser Pro Ala Ala Pro Lys Pro Thr Ser Lys
145 150 155 160

Pro Val Val Ala Lys Ser Ser Ser Ala Ser Lys Pro Ser Phe Val Pro
165 170 175

Lys Ser Thr Gly Lys Pro Val Ala Pro Ala Lys Pro Lys Pro Lys Asn
180 185 190

Ile Thr Lys Asp Ala Gly Trp Gly Asp Ala Glu Asp Val Glu Glu Arg
195 200 205

Asp Phe Asp Lys Lys Pro Leu Asp Asn Val Pro Ser Ala Tyr Lys Pro
210 215 220

Thr Lys Val Asn Ile Asp Glu Leu Arg Lys Gln Lys Ser Asp Thr Thr
225 230 235 240

Ser Ser Thr Pro Lys Thr Phe Lys Ser Glu Pro Gln Glu Glu Lys Asn
245 250 255

Asp Asp Asp Gly Gln Ser Lys Pro Leu Ser Glu Arg Met Lys Ala Tyr

260 265 270

Asp Gln Pro Ser Ser Ser Asp Gly Arg Leu Thr Ser Leu Pro Lys Pro
275 280 285

Lys Ile Gly His Ser Val Ala Asp Lys Tyr Lys Ala Ser Ala Ser Gly
290 295 300

Asn Gly Ala Ala Pro Ala Phe Gly Ala Lys Pro Ala Phe Gly Thr Gln
305 310 315 320

Ser Val Asp Ser Arg Lys Asp Lys Leu Val Gly Gly Leu Ser Arg Asp
325 330 335

Phe Gly Ala Glu Asn Gly Lys Thr Pro Ala Gln Ile Trp Ala Glu Lys
340 345 350

Arg Gly Lys Tyr Lys Thr Val Ala Ser Asp Glu Lys Glu Thr Asn Ser
355 360 365

Ser Glu Lys Val Asp Glu Pro Glu Glu His His Ala Ala Asp Leu Ala
370 375 380

Lys Lys Phe Glu Glu Lys Ala Asn Ile Ala Gly Asp Thr Pro Ser Leu
385 390 395 400

Pro Thr Arg Asn Leu Pro Pro Ala Pro Pro Ala Arg Glu Thr Ala Ile
405 410 415

Pro Ser Asn Glu Lys Asp Lys Xaa Glu Lys Glu Glu Glu Glu Gln Ala
420 425 430

Pro Ala Pro Ser Leu Pro Thr Arg Asn Leu Pro Pro Pro Ser Gln Arg
435 440 445

Gln Pro Glu Pro Glu Pro Glu Pro Glu Glu Glu Glu Glu Glu Glu Glu
450 455 460

Xaa Glu Ala Pro Ala Pro Ser Leu Pro Ala Arg Asn Leu Pro Pro Ala
465 470 475 480

Pro Lys Ala Glu Ala Glu Glu Ser Lys Lys Gln Ser Thr Thr Ala Thr
485 490 495

Ala Glu Tyr Asp Tyr Glu Lys Asp Glu Asp Asn Glu Ile Gly Phe Ser
500 505 510

Glu Gly Asp Leu Ile Ile Asp Ile Glu Phe Val Asp Asp Asp Trp Trp

515 520 525

Gln Gly Lys His Ala Lys Thr Gly Glu Val Gly Leu Phe Pro Ala Thr
530 535 540

Tyr Val Ser Leu Asn Glu Lys Ala Ala Asp Lys Glu Glu Glu Ala Pro
545 550 555 560

Ala Pro Ala Pro Ala Pro Ser Leu Pro Ser Arg Glu Glu Thr Gln Ala
565 570 575

Ala Pro Ala Leu Pro Ser Arg Ser Glu Gln Lys Pro Glu Ser Lys Thr
580 585 590

Ala Thr Ala Glu Tyr Asp Tyr Glu Lys Asp Glu Asp Asn Glu Ile Gly
595 600 605

Phe Ser Glu Gly Asp Leu Ile Val Glu Ile Glu Phe Val Asp Asp Asp
610 615 620

Trp Trp Gln Gly Lys His Ser Lys Thr Gly Glu Val Gly Leu Phe Pro
625 630 635 640

Ala Asn Tyr Val Val Leu Asn Glu
645